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February 3, 2003, 16:38:05; Search time 4703.97 Seconds (without alignments) 10165.006 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
                                                                    OM nucleic - nucleic search, using sw model
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

a: Chordata; Craniata; Vertebrata; Euteleostomi;	2406104	1643 bp DNA linear PAT 22-JAN-2001 Patent WO0078972.	ALIGNMENTS	AC131242 AC13142 Rattus AC111741 AC111741 Rattus	AC097674 AC097674 Rattus	AF429315 AF429315 AF429315	AC109982 AC109982	AX060898	AXU60713 AXU60721 AXU60721	AF285167 AF285167	AX060892 AX060892	AF26/202 AX060713 AX060713	AX139818 AX139818 AX139818	AX127831 AX127831	AK024328 AK02254	AXU92589 AX351032 AX351032	AX060894 AX060894	AX060715 AX060715	AX253452 AX253452	AX351029 AL359182	AX351031 AX351031	Ar28/26 AC125837 AC125837	AL807243 AL807243 AL807243 M	ACUZ1345 AF258627 AF258627	AC021246 AC021246 HOMG	AC021246 AC021246 HOMG	HSA252201 AJ252201 HOME	AF287262 AF287262 HOMG AC012230 AC012230 HOMG	AX351031 AX351031 Segv	AA331029 AA331029 SGG AF275948 AF275948 HOMG	AX092589 Sequ	AL359182 AL359182 Bum	AX060715 Seque	DB ID Description
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Lawn,R.M., Wade,D., Oram,J.F. and Garvin,K. Pate binding cassette transporter protein abol Patent: WO 0078971-A 3 28-DBC-2000;
CV THBRAPEUTICS, INC. (US)
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                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%;
Matches 1543; Conservative 0;
THERAPEUTICS, INC.
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Submitted (II-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, JK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequest&sanger.ac.uk Clone requests: clonerequest&sanger.ac.uk Clone requests: clonerequest&sanger.ac.uk Clone requests replaced $\forall \text{1812} \text{1468}.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlapping clone, as we submit sequences with this sequence was finished as follows unless otherwise noted: all regions were either couble-stranded or sequenced with an alternate
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Human DNA sequence from clone RP11-217B7 on chromosome 9, complete
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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chemistry or covered by high quality data (i.e., phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MIS subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw.; SWISSPRCT; Tr., TREMBL; WP:, WORMPEP; Information on the WORMPEP database can be found at.
                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  derived from a single pUC clone. Restriction digest data confirm the assembly."
                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/HGP/Chr9
SM11-27787 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                IMPORTANT: This sequence is not the entire insert of clone stri-2.787 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true right end of clone RPII-21787 is at 96717 in this sequence. The true left end of clone RPII-12780 is at 2000 in this sequence. The true right end of clone RPII-122F10 is at 72980 in this sequence. The true right end of clone RPII-31326 is at 2000 this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Sequence from reads from a short insert library derived from a single_pUC clone. Restriction digest data
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 TAGCATGGAGGGGGCTTGT-CAGCTGAATGTCTGTATGCAGGTGGTGGAGTTCTGGAAT 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Sequence from AF275948 sequenced by National Institutes of Heath, National Heart, Lung and Blood Binstitute Bethesda, MD 20892, USA." 84278 A84240. 84278 A6427 A6427 A6427 A6427 A6427 A6427 A6427 A6427 A6427 A6427
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/note="Sequence from reads from a
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/db_xref="taxon:9606"
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/clone="RP11-217B7"
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Aventls Pharma S.A. (F3)
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                             AACCTCTGCGCTCGGTGCAGCCGAATCTATAAAGGAACTAGTCCCGGCAAAAACCCCGGT
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Sequence 1 from Patent WO0183746.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1021
                                                                                                                                                                                                                               1939 CCAAAGGCAAACAGAGAAGTTGGAGGTCTGGAGTGGCTACATAATTTTACACGACTGCAA 1998
                                                                                                                      610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  901
                                                                                                                                                                                                                                                                                                                                                         CCIACTCTTGCCTTTTTTTGCCCCTCCAGTGTTTTGGGTAGTTTTGCT-CCCCTACAG
                                                                                                                                                                                                                                                                                    1999 ITCTCIGGCTGCACTTCACAAATGTATACAAACTAAATACAAGTCCTGTGTTTTTTTATCAC
                                                                                                                                                                                                                                                                                                                                                                                                              2118 TIGHTEGTIGGITTGITTGITTGITTTTGITTTTGIGGCCTCCTCCTCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTACAGAGTCTGCGGCGCAGCCCGGAGCCCAGCGCTTCCCGGGGGTCTTAGGCCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----CCCCACCCCACCCACCTCCCCCAACTCCCTAGATGTGTCGTGGGGGGGCTGAACS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1377 ICGCCCGTTTAAGGGGCCGGGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1437 TAAACAGAGGCCGGGAACGGGGGGGGGGAGGAGGAGGAGAGCATTGACGATAGTAA
2238 GGGAATCTCCAAGGCAGTAGGTCGCCTATCAAAATCAAAGTCCAGGTTTGTGGGGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRAAGGAAACAAAAGACAAAAAAAAATGATTGGCGTCCTGAGGGAGATTCAGCCTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTAGAGAGTCTGCGGCGCAGCCCCGAGCGCTTCCCGGCGCGTCTTAGGCCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCCGGGCGGGGAAGGGGACGCAGCGGGGACCCTAAGACACCTGCTGTACCCTCCAC
                                                  IAGTTTGTTGGCTTGATGACTTAAATATTTAGACATATGGTGTGTAGGCCTGCATT
                                                                   CCTACTCTTGCCTTTTTTTTGCCCCTCCAGTGTTTTGGGTAGTTTTGCTCCCCCTACAG
                                                                                                                                                                                             INCICIGGCIGCACITCACAAATGIAIACAAACIAAAIACAAGICCIGIGIIIITAICAC
                                                                                                                                                                                                                                                                                                                                          AGGGAGGCTGATCAATAAAAGAATTAAAAGGGGGCTGGTCCCCATAITGTTCTGTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACAAAAGCAGCCCATTACCCAGAGGACTGTCCGCCTTCCCCCTCACCCCAGCCTAGGCCT
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join(25994 25989, 40385, 40478,45012, 45153,46423, .46541, 67729 (57924, 25988, 40385, 40478,45012, .45153,46423, .46541, 67729 (57926, 25981, .71007,83960, .84052,89010, .89350, 81062, 92101,92433, .95494,96678, .96652,97102, .97907, 936428, .98604,100391, .100613,102360, .102861,103642, .103846, 104460, .105064,106862, .100703,108023, .108154, .110946, .110946, .110946, .110946, .110946, .110946, .110946, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .110964, .11096
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KLEPIATEVWIINKSWELLDERKFWAGIVFTOTTPGSIELPHHVKYKIRMDIDNVERT
NYTROSYMDOPPRADPFBDMRVWQGFRYLQDVVGQAIIRVLTGTEKKTGVYMQMFY
PCYVDDIFLRYMSRSMPLFWILANISSVAVIIKGIVYEKEAFLKETMRIMGLDNSILW
FSWFISSLIPLLVSGAGLLVVILKLGNLLPYSDPSVVFVFLSVFAVTILQCFLISTLE
SRANIAAACGGIIYFTIYLLYULCVAMQDYVGFTLKIFAXLLGSPVAFGCECEFFALFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAXKOMKKHLKLAKDSSADRËTNSLGRPMTGLDTRNNVKVWFNNKGWHAISSFLNVIN
NAILRANJQKGENPSHYGITAFNHPLNLTKQQLSSVAXMTTSVDVLVSICVIFAMSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PASFVVFLÍQERVSKAKHLQFISGVKPVIÝWĪSNFVWDMCNYVVPATLVIIFICFQQ
KSYVSSTNLPVLALLLLIKGWSITPLKYPASFVFKIPSTAYVVLTSVNLFIGINGSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLKYRQGRTIILST
HHMDBADVLGDRIAIISHGKLCCVGSSLFLKNQLGTGYXLILVKKDVESSLSSGRNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GWKLTQQQFVALLMKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSLE
LQPAWYNEQYTFVSNOAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQAGEEEW
TTAPVPQTIMDLFQNGNWTWQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DILQDJIGRNISDYLVKTYVQIJAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQEVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MACOMPOLABLILMKNLTPRRROTCOLLLEVAMPLETFLILISVRL
SYPPYEQHECHEPNKAMPSAGTLPWVQGIICNANNPCFRYPTFGEAPGVVGNFNKSIV
ARLFSDARRLLLYSQKDTSMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFGGFLYH
NISLFKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEEMYQLGDGEVSELCGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REKLAABERVIRSNMDILKPILRTINSTSPPPSKELAEATKTILHSLGTLAQELFSNR
SWSDNRQEVNRTINVNSSSSSTQIYQAVSRIVCGHPEGGGLKIKSLNNYEDNNYKALF
GGNGTEEDAETFYDNSTTPYCNDLMKNLESSPISRIINKALKPILVGKILYTPDTPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYVLPYEAAKEGAFVELFHEIDDRISEYGISSYGISETTLEEIFLKVAEESGVDAETS
DGTIPARRRAFGDKQSCIRPFTEDDAADPNDSDIDPESRETDLLSGMDGKGSYQVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RQVMAEVNKTFQELAVFHDLEGMWEELSPKIWTFMENSQEMDLVRMLLDSRDNDHFWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDG-GVQWDNLFESPVEBDGFNLTTSVSMALEDTFLYGVMTWYLEAVFPGQYGIPRW
YFYCTKSYWRGEESDEKSHPGSNQKRISEIOMEEEPTHLKLGVSIQNLVKVYRDGMKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYILGKDIRSEMSTIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QNLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEKHVKAEMEQMALDVGLPSSKLKSKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STVSYLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNLTRKHVSEARLVEDIGHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAF86276.1"
/db_xref="GI:9247086"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="Alu"
25038. .25314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="Alu"
18600. .18860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="Alu"
20950. .21206
                                /rpt_family="Alu"
6615. .6877
                                                                                                                       /rpt_family="Alu"
8800. 9046
                                                                                                                                                                                                                             /rpt_family="Alu"
9998. .10279
                                                                                                                                                                                                                                                                                                                                    /rpt_family="Alu"
11859. .12133
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="Alu"
[2810. .12902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="Alu"
15220. .15399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="Alu"
[5508. .15787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/product="ABCA1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="Alu"
join(25924. .2598
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1 (bases 1 to 149034)
Santamarina-Pojo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L., Cheng,J.F., Osorio,J., Remaley,A., Yang,X.P., Haudenschlid,C., Prades,C., Chimini,G., Blackmon,E., Francois,T., Duverger,N., Rubin,B.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete genomic sequence of the human ABCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000) 20345099
                                                                                                            1557 INGCARGERARGIGARECEGRACESCARARGEGRACEGRACECTTCTCTCCCGG 1616
                                                                                                                                                                  2898 ITGCGAGGAGAGAGAGGGGCCGGGAGACCCCAGAGCCGAGCCGACCCTCTCTCCCGG 2957
     2838 CCTCIGCGCICGGIGCAGCCGAAICIATAAAAGGAACTAGTCCCGGCAAAAACCCGGTAA 2897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 149034)
Santamarina-Fojo,S., Peterson,K.M., Knapper,C.J., Freeman,J.A.
Remaley,A.T., Yang,X.-P., Haudenschild,C.C., Blackmon,E.E.,
Francois,T.L. and Brewer,H.B. Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (08-JUN-2000) Molecular Disease Branch, National
Institutes of Heath, National Heart, Lung and Blood Institute,
Bethesda, MD 20892, USA
1. 149034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO Sapiens ASCAl (ABCAl) gene, complete ods. AZ275948
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/gene="ABCAl"
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Aventis Pharma S.A. (FR)
                      1137 CCGCGCGTCTTAGGCCGGCGGGCGGGCGGGGGAAGGGGGAACGAGCGGGGGCCTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2178 TGAAGAGAGCAGTAAGATGTTCCTCTCGGGTCCTCTGAGGGACCTGGGGAGCTCAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1886 CCTACICTTGCCTTTTTTTTTGCCCCTCCAGTGTTTTGGGGTAGTTTTGCT-CCCCTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAAAGGCAAACAGAGAAGIIGGAGGCTCIGGAGTGGCIACAIAAITITACACGACTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCTCTGGCTGCACTTCACAAATGTATACAAACTAAATACAAGTCCTGTGTTTTTATCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  731 AGGGAGGCTGATCAATATAATGAAATTAAAAGGGGGCTGGTCCCATATTGTTCTGTTTT
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                                                                                                                                                                                                                                                                               AGATICATATITAGACICTICACAGITIGACCIGAGITITGGCCAGAATAAGGIGACAIT
                                                                                                                                                                                                                                                                                                                       1762 AGAITCAIAITTAGACTCTTCACAGTTTGACCTGAGTTTTGGCCAGAATAAGGIGACAIT
                                                                                                                                                                                                                                                                                                                                                                          TAGITIGITGCCITGATGACTTAAATATTTAGACATATGGTGTGTAGGCCTGCATT
                                                                                                                                                                                                                                                                                                                                                                                                551 CCTACTCTTSCCTTTTTTTTGCCCCTCCAGTGTTTTGGGTAGTTTTGCTCCCCTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAAAGGCAAACAGATAAGITGGAGGTCTGGAGTGGCTACATAATTTTACACGACTGCAA
                                                                                                                                                                                                                                 GCCTGCTIGGGCCTCTTCTACGGGTCTGTCCTGAGTCTTCTATGAAT---CCTTCAGGGC
TTCTGGCCAAACTCAGGTCAAACTGTGAAGAGTCTAAATGTGAATCTGCCCTTCAAGGT
                                                                                                                                                                                     GCCIGCII - GGCCICITCIACGGGICTGICCIGAGICIICTAIGAATCICCCIICAGGGC
                                                                                          GSCTACAAAGGTATCTTTGTCAAGGTAGGAGACCTTGTGGCCCTCCACGTGCACTTCCAGG
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NRFGDGYTIVVRIAGSNPDLKPVQDFFGLA?PGSVLKEKHRNMLQYQLPSSLSSLARI
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KLEPTATEVWLINKSMELLDERKFWAGIVFTGITFGSIELPHHVKYKIRMDIDNVERT
NKIKDGYWDPGPRADPFEDMRYWGGFAYLQDVVEQAIIRVLTGTEKKTGVYMQMPY
PCYVDDIFLRVMSRSWPLFWTLAMIISVAVIIKGIVYEKEARLKETMRIMGLDNSILW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSWFISSLIPLLVSAGLLVVILKLGNILPYSDPSVVFVFLSVFAVVTILQCFLISTLF
SRANLAAAGGGIIYFTLYLPYVLCVAWQDYVGFTLKIFASLLSPVAFGFGCEGFALFE
EQGIGVQWDNLFESPVEEDGFNLTISVSMMLFNTFLYGVMTWYIBAVFPGGYGIPRPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLSWDLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARLFSDARRLLLYSQKDTSMKDMRKYLRTLQQIKKSSSNLKLQDFLYDNBTFSGFLYH
NLSLPKSTYDKMLRADVILHKVFLQCYQLHLTSLCNGSKSEBMIQLGDQBVSELCGLP
XEKLAAABRYLRSNWDILK?ILRTLNSTSPFPSKBLABATKILLHSLGTLAQELFSMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWSDYROEVÆLTYVNSSSSSTÇIYQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALÆ
GGNGTEEDAETFYDNSTTPYCNDLMKNLESSPLSRIIMKALKPLLVGKILYTPDTPAT
ROVMAEVNKIFQELAVFHDLEGMWEELSPKIMTFMENSQEMDLVRMLLDSRDNDHFWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MACWPQLRLLJWKNLTFRRRQTCQLLLEVAWPLFIFJILISVRL
SYPPYEQHECHFPNKAMPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="ATP-binding cassette 1 sub-family A member 1"/protein_id="AAX43526.1"
join(58411. .58476,72893. .72986,77520. .77661,7893
101048. 101169,104152. 104328,11787. 117375.
123329. 122569,125285. 125424,125754. 125876.
130079. 130276,131023. 131228,131749. 131925.
138268. 138381,140179. 140350,441440. 131925.
14277. 142919,143123. 143269,136959. 137163.
14571. 148884,150280. 150428,13637. 144877.
153438. 15356,156588. 15677,158278. 158372.
153438. 15356,156588. 156797,158278. 158372.
163013. 163182,164413. 164590,165888. 166703.
16488. 174589,174961. 177079,171087. 172093.
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1C1048. .10116
/gene="ABCA1"
/:umber=6
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72893. .72986
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77520. .77661
/gene="ABCA1"
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/qene="ABCA1"
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78931. .79
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                          CDS
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Berkeley National Laboratory, 1 Cyclotros Rd, MS 84-171, Berkeley,
CA 94720, USA
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/gene=7.Abc.Ar
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Mammalia: Eutheria; Primates, Catarrhini; Hominidae; Homo.
1 (bases 1 to 201144)
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                                                                   ----ceceaeceaeceaecrececeaacrecetaargigues ----
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                                                                                                                                                                                                                                    1377 TOGCCOGTTTAAGGGGCGGGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTACA 1436
                                                                                                                                                                                                                                                                                                   2718 TCGCCCGTTTAAAGGGGCGCCCGGCTCCACGTGCTTTCTGCTGAGGAGTAACA 2777
                                                                                                                                                                                                                                                                                                                                                                                                           1437 TAAACAGAGGCCGGGAACGGGGGGGGGGGGGGGGGGGGCACAGGCTTTGACCGATAGTAA 1496
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jiu,Y., Cavelier,L., Chiu,S., Yang,X., Rubin,E. and Cheng,J.F.

Human and mouse ABCAl comparative sequencing and transgenesis

studies revealing movel regulatory sequences

Genomics 73 (1), 66-76 (2001)
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                                                                                                                .181457
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Qiu,Y., Caveller,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
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/db_xref="taxon:9606"
33931. 181457
/gene="ABCA1"
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176625. 176717,1
/gene="ABCA1"
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/gene="ABCA1"
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Homo sapiens clone RPll-1M16, WORKING DRAFT SEQUENCE, 39 unordered
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 175064)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33635 GCCCGGGCGGGGGAAGGCACGCAGGCAGGGGAACCCTAAGACACCTGCTGTACCCTCCAC 33694
                                                                                                                33574
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                       1262 GCCCGGGCGGGGAAGGGGGACGCAGACGCGGACCCTAAGACACCTGCTGTACCCTCCAC 1321
1022 ITGAAAGGAAACAAAAGACAAGACAAAATGAITGGCGICCTGAGGGAGAITCAGCCIAGA 1081
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                                                                                              1082 GCTCTCTCCCCCAATCCCTCCCGCTCAGGAAACTAACAAAGGAAAAAAATTG
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Homo sapiens, clone RP11-1M10
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wasaliev, S., Taramas, J., Wasaliev, M., Wo, A., Wheeler, J., Wu, X., Wasaliev, H., Wo, A., Wheeler, J., Wu, X., Talamas, J., Ta
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Center: Whitehead Institute/ MIT Center for Genome Research
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Insert size: 171284; sun-of-contigs
Quality coverage: 2.9 in 020 bases; agarose-fp
Quality coverage: 3.2 in 020 bases; sun-of-contigs
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Contact: sequence_submissions@genome.wi.mit.edu
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28184: contig of 2377 bp in length
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138060 138159: gap of 10
138160 145491: contig of 17
145492 145591: gap of 10
145592 157391: contig of 11
15332 15749: gap of 10
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/db_xref="taxon:9606"
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  45448: contig of 2
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Porsach Carumann, Langaran, T., Ediment, S., Borsukova, H.,
Porsach-Ozcurumez, M., Langaran, T., Ediment, S., Borsukova, H.,
Raminski, W.E., Drobatk, W., Honer, C., Schumacher, C. and Schnitz, G.
The zinc finger protein 202 (2NF202) is a transcriptional repressor
of ATP binding cassette transporter A1 (ABCA1) and ABCG1 gene
expression and a modulator of cellular lipid efflux
J. Biol. Chem. 276 (15), 12427-12433 (2001)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Function="cholesterol efflux regulatory protein"
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                                                           HSA252201 1167 bp DNA linear PRI l
Homo sapiens partial ABC-1 gene for ATP-binding cassette
transporter-1, 5'UTR and promoter region.
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AJ252201.1 GI:12053757
ABC-1 gene; ATP-binding cassette transporter-1; promoter.
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/db_xref="taxon:9606"
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/cell_type="leukocyte"
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Porsch-Oezcueruemez,M.K.
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AUTHORS
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/function="cholesterol efflux regulatory 315 c 327~g 247~t
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                                               Score 1006; DB 9;
Pred. No. 1.8e-257;
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Mammaila; Butheria; Primates; Catarrhini; Hominidae; Bomo.
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Homo sapiens clone RP11-1N10, LOW-PASS SEQUENCE SAMPLING.
AC021246
AC02146 GI:9119882
HTG: ETGS PERATO
926 CCTATCAAAATCAAAGTCCAGGTTTGTGGGGGAAAACAAAAGCAGCCCATTACCCAGA
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Homo sapiens chromosome, clone RPli-1N10
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100 bp 855 bp

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35204. Contig of 835 bp in length 15304. gap of 100 bp 36156. contig of 835 bp in length 5256. gap of 100 bp 228. gap of 100 bp 31080. contig of 872 bp in length 88.9 gap of 100 bp 38083. contig of 885 bp in length 39083. contig of 855 bp in length 39083. contig of 855 bp in length 39031.
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contig of 848 bp in length
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contig of 855 bp in ab of 100 bp
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33312: contig of 944 bp
12: gap of 100 bp
34268: contig of 856 bp
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28532: contig of 856 bp
32: gap of 100 bp
29492: contig of 860 bp
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       Ferretra, P. FitzHugh, W. Forrest. C. Gage, D. Galagan, J. Garciya, P. FitzHugh, W. Forrest. C. Gage, D. Galagan, J. Garciya, S. Grant, G. Hagos, B. Heaford, A., Horton, L. Howland, J. C. Johnson, R., Jones, C. Kann, L. Karatas, A. Klein, J. Landers, T. Lenders, R. Lieu, C. Liu, G. Lock, K. Macdonald, P. Marquis, N. Meneus, L. Mocurk, A., McKerna, K. McPheeters, R., Meldrim, J. Meneus, L., Morrow, J., Naylor, J. Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M. Petrason, K., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J. Zammer, A. and Zody, M.
                                                                                                                                                                                        Center for Genome
11, USA
                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                      Submitted (16-7AN-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 13, 2000 this sequence version replaced gi:6705871. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
Doyle, K., Fenestor, J.,
                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This record contains 73 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be generich and allows
* overlap relationships among clones to be deduced.
* fowever, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                                                                                                           Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepearMasker.html
                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
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Web site: http://www-seq.wi.mit.edu
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41649 GGAGCTC 41655
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63827: contig of 861 bp in length
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2.5e-127;
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Gardynn, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Landers, T., Lehoczky, J., Lievine, R., Liew, C., Liu, G., Locke, K.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,
Norman, C.B., O'Connor, T., O'Donnell, P., Olivar, T.M., Pererson, K.,
Pierre, N., Pisani, C., Polnara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, P., Spencer, B., Starge-Thomann, M.,
Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
Direct, Submission, A., Chiller, M., Man, M., Rother for Genome
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: sequence.submissions@genome.wi.mit.edu
                                                     1577 GGCCGGGACCCGCAGAGCCGACCCTTCTCTCCCCGGGTGCGCCAGGGCAGGGCGG 1636
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Homo sapiens clone RP11-1N10, LOW-PASS SEQUENCE SAMPLING.
AC021246
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http://ftp:genorie.washington.edu/RM/RepeatMasker.html
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens Chromosome, clone RP11-1N10
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Ouery Match 16.5%; Score 271.6; DB 2; Length 69570; Best Local Similarity 89.8%; Pred. No. 4.9e-61; Matches 289; Conservative 0; Mismatches 33; Indels 0; Gaps

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                                                                                                                                                                                                                                                                                                                                                                                HTG 13-JUL-2000
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Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gis6705761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
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Center: Whitehead Institute/ MIT Center for Genome Research
                67522 AGAGCCCGGCAACGGGGGGGGGGGGGGGGGGAGCACCAGGCTTTGACTGATAGTAACTTCT
                                                                                                                                          1502 GCGCTCGGTGCAGCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCGGTAATTGCG
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                                                                                                                                                                                                                                                                                                                                                                   ACUZI345 1 1 10698 bp DNA linear HTG l
HOMO Sapiens clone RPli-24J9, LOW-PASS SEQUENCE SAMPLING.
AC021345
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http://fip.genome.washingion.edu/RM/RepeatMasker.html
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
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Smit, A.F.A. & Green, P. (1996-1997)
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Unpublished
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RESULT 14 ACO21345/c LOCUS DEFINITION ACCESSION

ORGANISM

KEYWORDS VERSION

REFERENCE

JOURNAL REFERENCE TITLE JOURNAL

COMMENT

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74456: gap of 100 bp 105 bp 10
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f 927 bp in length
100 bp
f 898 bp in length
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ARZJUGZ/ 697 bp mRNA linear PRI 11-MAY-2000 HOMO Sapiens ATP binding cassette transporter 1 (ABCA1) mRNA, partial cds.
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E 1 (bases 1 to 697)

S Pullinger.C.R.; Hakamata, H., Duchateau, P.N., Eng.C.,
Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
Analysis of hABCl gene 5' end: additional peptide sequence, promoter region, and four polymorphisms

E 2 (bases 1 to 697)

S Pullinger.C.R.; Hakamata, H., Duchateau, P.N., Eng.C.,
Aouizerat, B.E., Fielding, C.J. and Kane, J.P.

Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                    GGCTCCACGTGCTTTCTSCTGAGTGACTGAACTACATAAACAGAGGCCGGGAACGGGGCG
                                                                                        Length 90698;
68947: gap of 100 bp

68934: contig of 887 bp in length

69034: gap of 100 bp

69910: contig of 876 bp in length

70010: gap of 100 bp
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ed. No. 7.5e-50;
Mismatches 141;

    .697
    /organism="Homo sapiens"
/db_xref="taxon:9606"
    /chromosome="9"

                                                                                         Score Pred. 1
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AUTHORS
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KEYWORDS
SOURCE
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// 1996 - 1997
// gene="ABCAl"
// note="membrane-bound"
// note="membrane-bound"
// product="ATP binding cassette transporter 1"
// protein_id="AAF069513.1"
// brotein_id="AAF069513.1"
// brotein_id="AAF069513.1"
// translation="WACWPQLRLLLWKNLTFRRRQTCQLLLEVAWPLFIFLILISVRLSYPYEQHECHFPNRAMPSAGTLPWVGIICNANNPCFRYPTFGEAPGVVGNFNKS"
a 198 c 190 g 156 t 1 others
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Search completed: February 4, 2003, 00:59:00 Job time : 5346.97 secs

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3, 2003, 16:38:05; Search time 397.962 Seconds (without alignments) 10165.006 Million cell updates/sec US-09-596-141C-3_COPY_1394_1532 139 1 999ccccggctccacgtgct......agccgaatctataaaaggaa 139 4109280 Total number of hits satisfying chosen parameters: 2054540 segs, 14551402878 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY_NUC Capop 10.0 , Gapext 1.0 em_un:*
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	36	E)	, (T)	8735	N	AC068886	386 Ното
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FEATURES

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AC021246 69570 bp DNA linear HTG 13-JUL-2003
Homo sapiens clone RP11-1N10, LOW-PASS SEQUENCE SAMPLING.
AC021246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1643)
Lawn, R.M., Wade, D., Oram, J.P. and Garvin, M.
Atp binding cassette transporter protein abel polypeptides
Patent: Wo 0078971-A 3 28-DEC-2000;
CV THERAPEDTICS, INC. (US)
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Fomo.
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                 Pred. No. 1.1e-31;
Mismatches 0;
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100.0%; Pred. No. 1.1e-31;
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           The zinc finger protein 202 (ZNF202) is a transcriptional repressor of ATP binding cassette transporter AI (ABCA1) and ABCG1 gene expression and a modulator of cellular lipid efflux 1. Biol. Chem. 276 (15), 12427-12433 (2001)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Lawn, R.M., Wade, D. and Garviz, M.

Regulation with binding cassette transporter protein abcl

Patent: WO 0778972-A 3 28-DEC-2000;

CV THERAPUTICS, INC. (US)
                                                                                                                        2 (bases i to 1167)
Porsch-Oezcueruemez, M.K.
Direct Submission
Submitted (05-3AN-2000) Porsch-Oezcueruemez M.K., Institute for Clinical Chemistry, Universitiy of Regensburg,
FRanz-Josef-Strauss-Allee 11, 93042 Regensburg, GERMANY
1.01167
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35204: contig of 836 bp
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18041: contig of 869 bp
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contig of 827 bp
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                                                                                                                                                                                                                                                             Genome
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                         Submitted (16-JAN-2000) Whitehead Institute/MIT Center for (Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6705871. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This record contains 73 individua.
sequencing reads that have not been assembled into contigs. Runs of Nare used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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regether with a note of the everlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with colly a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either couble-stranded or sequenced with an alternate chemistry or covered by high quality date (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, BMBL: Sw:,
                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
 Cambridgeshire, CBIO 15A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerecuest@sanger.ac.uk
On Jan 15, 2002 this sequence version replaced gi:18121468.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                        Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrg http://www.sanger.ac.uk/HGP/Chrg http://www.sanger.ac.uk/HGP/Chrg http://www.sanger.ac.uk/HGP/Chrg of RPII-212R7 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                               SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
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Human DNA sequence from clone RP11-217B7 on chromosome 9, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 96717)
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Direct Submission
Submitted (ll-JaN-2002) Welicome Trust Sanger Institute, Hinxton,
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                                                            IMPORTANT: This sequence is not the entire insert of clone RP11-217B7 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true right end of clone RP11-127B7 is at 9677 in this sequence. The true left end of clone RP11-122F10 is at 72980 in this sequence. The true right end of clone RP11-122F10 is at 2000
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Institutes of Hearh, National Heart, Lung and Blood
Institute, Bethesda, MD 20892, USA."
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http://www.chcri.org/bacpac/home.htm
VECTOR: pBACe3.6
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29 15328; gap of 100 bp 17200: contig of 1872 bp in length 101 17300: gap of 1800 bp 20 20131: contig of 2831 bp in length 102 20131: gap of 100 bp 100 bp 132 22587: contig of 2356 bp in length 100 bp 100 
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                                                                                                                                                                                                                                                                 AC012230 175064 bp DNA linear HTG 22-APR-2000 Earo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered
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Submitted (21-007-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 22, 2000 this sequence version replaced gi:6454033.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 175064)
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Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Quality coverage: 3.2 in Q20 bases; sum-of-contigs
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project information
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------ Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
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HTG; HTGS_PHASE1; FTGS_DRAFT
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Homo sapiens
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AC012230
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I bases: 1 to 1167)

Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,

Aouizerat, B.D., Fleidang, C.J. and Kare, J.P.

Analysis of hABCl gene 5' end: additional peptide sequence, promoter region, and four polymorphisms

Piochem. Biophys. Res. Commun. 271 (2000) In press
2 (bases 224 to 1167)

Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
                                                                                                                                                                                                                                                                       Eukaryota, Metazoa: Ciordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 183999)
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                                                                                                                                                                                                                                                                                                                       Hayden M.R., Brocks-Wilson, A.R., Pimstone, S.N. and Clee, S.M. Compositions and methods for modulating hdl cholesterol and triglyceride leaven. Patent: WO 0115676-A 1 08-MAR-2001; University of British Columbia (CA); Xenon Genetics Inc. (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nr.2002.451 1167 bp DNA linear PRI 23-JUN Homo Sapiens ATP binding cassette transporter 1 (ABCA1) gene, promoter and exon 1.
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                                                                                                                                                  Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 139; DB 6;
ilarity 100.0%; Pred. No. 6.8e-32;
Conservative 0; Mismatches 0;
                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                               /crganism="Homo sapiens"
/db_xref="taxon:9606"
% 37944 c 41170 g 54950 t
                                                                                                                                         Sequence 1 from Patent W00115676.
AX092589
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                        3623 GCCGAATCTATAAAAGGAA 3641
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/db_xref="taxon:9606"
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Dullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Aouizeaat, B.E., Fielding, C.C. and Kane, J.P.
Direct Submission
Submitted (23-JUN-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San Francisco, CA 94143-0130, USA
Sequence update by submitter
O: Jun 23, 2000 this sequence version replaced gi:7769713.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S.
Regulatory nucleic acid sequences of the abol gene
Patent: WO 0183746-A 3 08-NOV-2001:
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Pred. No. 3.3e-31;
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llarity 99.3%; Pred. No. 3.7e-31;
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/db_xref="taxon:9606"
/chromosome="9"
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Complete genomic sequence of the human ABCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
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Cheng,J.F., Oscrio,J., Remaley,A., Yang,X.P., Haudenschild,C.,
Prades,C., Chimini,G., Blackmon,E., Francois,I., Duverger,N.,
Rubin,E.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Deneile, P., Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S. Regulatory nucleic acid sequences of the abol gene Patent: Wo 0183746-A. 108 NOV-2001; Aventis Pharma S.A. (FR)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 149034)
2735 GGGCCCGGCTCCACGTGCTTCTGCTGAGTGACTACATAAACAGAGGCCGGGAA 2794
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llarity 99.3%; Pred. No. 3.3e-31;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                       DNA
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/db_xref="taxon:9606"
1 773 c 876 g 777
                                                                                                                                                                                                                                                                         Sequence 1 from Patent W00183746.
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AF275948
AF275948.1 GI:9247085
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                                                                                                                                       2855 GCCGAATCTATAAAGGAA 2873
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                                                                                  GCCGAATCTATAAAGGAA 139
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/rpt_family="Alu"
31050, 31314
/rpt_family="Alu"
31692, 31973
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36167. .36440
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                                142646. .14273
/qene="ABCA1"
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Remaley, A.T., Yang, X.-P., Haudenschild, C.C., Blackmon, E.E., Francois, T.L. and Brewer, H.B. Jr.
Direct Submission
Submitted (08-270N-2000) Moiecular Disease Branch, National Institutes of Heath, National Heart, Lung and Blood Institute, Bethesda, MD 20892, USA
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                                                                                                                                                                                                            /organism="Homo sapiens"
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1454. .148034
/gene="ABCA1"
                                                                                                                                                                Location/Qualifiers
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/rpt_family="Alu"
20950. .21206
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5563. .5839
\frac{1}{\sqrt{rpt_{\rm c}}} family="Alu"
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35038. .2531
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9998. .10279
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1859. .12133
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2810. .12902
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NLSLPKSTVDKKLRADVILHKVFLQGYQLHLTSLCNGSKSEEMIQJGDQEVSELCGLP
REKLAAAERVLRSNMDILKPILRTLNGTSPFPSKELABATKTILHSLGTLAQELFSMR
SWSDMRQEVWPLTNVNSSSSSTQIYQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALF
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EQGIGVQWDNLFESPVEDGFNLTTSVSMALPDTFLYGVATWY IEAVFPGQYGIPRPW
YFPCTKSYWFGBESDEKSHPGSNQKRISBICMEBEPTHLKLGVSIQNLVKVYRDGMKV
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SKYSSTRLÍFLYVLALLLÍLYGGSITPLHKTPASPYKFRIÐETAVVUTSVNDIGINSSVA
TFVLELFIDNKLNN NDILKGYFIIFPHTCLGRGLIDDWKNQAMADALERFGENRFVS
PLSWDLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVNAKLSFLNDEDEDVRRERQ
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PEKEVGKVGEWAIRKLGLVKYGEXYAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTG
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NRFGDGYTIVVRIAGSNPDLKPVQDFFGLAFPGSVXKBKHRNMLQYQLVBSSLARI
FSILSQSKKRLHIEDYSVSQTTLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLT
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ARLFSDARRLLLYSQXDTSMKDMRKVIRTLQQIKKSSSNLKLQDFLVDNETFSGFLYH
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DGTLPARRNRRAFGDKQSCLRPFTEDDAADPNDSDIDPESRETDLLSGMDGKGSYQVK
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TTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTA
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QQLDGLDWTAQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNGAIRTESRFKECVNLN
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FSWFISSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFVFLSVFAVVTILQCFLISTLF
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SQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLKYRQGRTIILST
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NKIKDGYWDPGPRADPFEDWRYVWGGFAYLQDVVEQAIIRVLTGTEKKTGVYMQQMPY
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40469. .140610,140982. .141116,142060. .142163,42646. .142738,143397. .143640,144581. .144721)
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Join(58411. .56476,72893. .72986,77520. .77661,78931. .79049, 101048. .101169,104152. .104328,117287. .117379, 122329. .122569,125285. .125424,125754. .125870, 130079. .130276,131023. .1312881,13149. .131925, 1317163, 1318288. .1318381,140179. .1312898,139959. .137163, 14477. .142919,143123. .143080,141340. .144471, 14277. .142919,143123. .143080,141837. .148884,102280. .1502280. .1502280. .1502280. .1502280. .1502280. .1502280. .1502280. .150372, 162491.
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SYPPYEQHEGHPPNKAMPSAGTLDWYGOTICNNNPCRPYPPEGAPGVGNPRKSIV
ARLFSDARTLLLYSQCDTSWKDMRYLRTLQQIKKSSSNLKLODFLUNNETFSGFLYH
NLSLPRSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEEMIQLGDGEVSELCGLP
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AVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYILGKDIRSEMSTIR
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GGNGTEEDAETFYDNSTTPYCNDLMKNLESSPLSRIIWKALKPLLVGKILYTPDTPAT
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FSWFISSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFVFLSVFAVVTILQCFLISTLF
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SQLSGGMQRKLSVALAFVGGSKVVILDEPIAGVDPYSRRGIWELLLKYRQGRTIILST
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NKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDYVEQAIIRVLTGTEKKTGVYMQQMPY
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      National Laberatory, 1 Cyclotron Rd, MS 84-171, Berkeley,
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/protein_id="AAK43526.1"
/db_xref="GI:13876613"
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166813. 166599,168502. 166588. 166703,
170109. 170229,171017. 17,7079,171987. 1722093,
174448. 174589,174961. 175095,176639. 176142,
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                                                Location/Qualifiers
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/gene="ABCA1"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 201144)
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Qiu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                               /rpt_family="HERV"
61246. .61489
44349. .44626
/rpt_family="Alu"
48473. .48669
/rpt_family="Alu"
50547. .50514
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58501. .sR@35
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62812. .63077
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69481. .59760
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55029. .55226
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72244. .72501
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NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVDVLVSICVIFAMSFV
STVSYLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNLIRKHVSEARLVEDIGHEL
TYVLPYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEEIFLKVAEESGVDAETS
                                                              LQPWWYNEQYTFVSNDAPEDTGTLELLNALTKDPGFCIRCMEGNPIPDI PCQAGZEEW
TTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKNLPVCPPGAGGLPPPQRKQNTA
                                                                                                                                                PASFVVFLIQERVSKAKHLQFISGVKPVIYWLSNFVWDMCNYVVPATLVIIFICFQQ
KSYVSSTNLPVLALLLLXGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVA
                                                                                                                                                                                 T=VLELFTDNKLNNINDILKSVFLIF9HFCLGRGLIDMVKNQAMADALERFGENRFVS
PLSWDLVGRNLFAMAVEGVVFF1TTVLIQYRFFIRPRPVNAKLS91NDEDEDVRRERQ
                                                                                                                                                                                                                                                   PEKEVGKVGEWAIRKLGLVKYGEKYAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTG
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NRFGDGYTIVVRIAGSNPDLXFVQDFFGLAFPGSVLKEKHRNMLQYQLPSSLSSLARI
                                               GWKLIQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSLE
                                                                                                 DILQDLTGRNISDYLVKTYVQITAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQEVN
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                                                                                                                                                                                                                                LTGDTTVTRGDAFLNKNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGV
                               OGTLPARRNRRAFGDKQSCLRPFTEDDAADPNDSDIDPESRETDLLSGWDGKGSYQVK
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda. F., Boylaslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choppel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzEugh, W., Forrest, C., Gage, D., Galagan, J.,
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Birrer, B., Lintoc, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome, clone RP11-1N10 |
Unpublished
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                    142777. .142919
/gene="ABCA1"
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/gene="ABCA1"
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36156: cont
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Gardyna, S., Grant, G., Hagos, B., Beaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Kiein, J.,
Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
McDhenelars, R., Medrils, J., McEwan, P., McGurk, A., McKernan, K.,
McPheeters, R., Melorim, J., Meneus, L., Morrow, J., Nay.or, J.,
Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, X.,
Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thoman, N.,
Tirrell, A., Vassiltev, H., Viel, R., Vo, A., Wyman, D., Ye, W.J.,
Zimmer, A., and Zody, M.,
                                                                                                                                                                                                          Genome
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                                                                                                                                                                                                   Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 13, 2000 this sequence version replaced 91:6705871. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overiap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion In the event that
                                                                                                                                                                                                                                                                                    http://frp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is updated, the accession number will
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Jap of 100 bp in length
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Web site: http://www-seg.wi.mit.edu
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16123: contig of 827 bp
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Direct Submission
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Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguslavkly,L., Boukhgalter,B., Brown,A., Burkert,G., Castle,A.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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HOMO sapiens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING
AC021345
                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 69570;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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867 bp in leagth
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llarity 94.2%; Pred. No. 5.8e-28;
Conservative 0; Mismatches 8;
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f 852 bp 3
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59082: contig of 852 c
59182: gap of
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Perreira,P., FitzEugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Landers,T., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marculis,N., McBwan,P., McGurk,A., McKernan,K.,
NCPHeeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
Pierre,N., O'Connor,T. C'Donnell,P., Olivez,T.M., Pererson,K.,
Pierre,N., Pisari,C., Pollera,V., Raymond,C., Rilby,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomanon,N.,
Slojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Firell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
                                                                                                                                                                                                                                   Zimmer.A. and Zody.M.

Direct Submission
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6765761.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                        Research
                                                                                                                                                                                                                                                                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This record contains 92 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project Information
Center project name: L4483
Center clone name: 24_J_9
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56 8855: app of 908 bp in length
6 9753: contig of 898 bp in length
4 9853: gap of 100 bp
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3: contig of 898 bp in length
100 bp.
7: contig of 904 bp in length
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100 bp.
2: contig of 875 bp in length
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11833 12739: contig of 907 bp in length
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5677: contig of 915 bp in length
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f 843 bp i
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2824: contig of Bp
2924: gap of 100 bp
3802: contig of Bre L
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8755: c. 5.
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Pred. No. 5e-24;
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64026: contig of 904 bp
64126: gap of 100 bp
65015: contig of 889 bp
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56165: contig of
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Direct Submission
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contig of 880 bp in
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                                                                                                                                                                                                                                                                                                                                                                                                                                   23568: contig of 889 by ir
668: gap of 100 bp
4554: contig of 886 by ir
654: gap of 100 bp
25521: contig of 867 bp ir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5587: gap of 100 bp 27464: contig of 877 bp ir 28466: contig of 902 bp ir 556; gap of 100 bp 
                                                                                                                                                                      ap of 100 by 100
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866 bp
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51209; contig of 859 bp
51309; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57: gap of 100 bp
44356: contig of 899 bp
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                       7679 17778: gap of 100 bp
7779 18679: contig of 901 bp
8680 18779: gap of 100 bp
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contig of 888 bp
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35433: contig of 898 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2: gap of 100 bp 8402: contig of 880 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p of 100 by contig of 927 bp
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45325: contig of 869 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02: gap of 100 bp
48293: contig of 891 bp
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contig of 870 bp
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contig of 907 bp
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contig of 898 5p
                                                                                                                                       centig of 853 pp
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26487: contig of
contig of
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46305: م
                                                                     coni
.: gap of
19632; ~
32
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33447: --
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41405: cont
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43357
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40467
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37422:
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9380: conf
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21620: con
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27464: .
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Length 90698;

100 bp 904 bp in length

in length

in length

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100 bp f 859 bp

Indels

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AL807243 186889 bp DNA linear HTG 30-JCN-2002 Mus musculus chromosome 4 clone RP23-25D17, *** SEQUENCING IN PROGRESS ***, 24 unordered pieces. Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 186889) Submitted (29-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UX. E-mail enquiries: camparager.ac.uk Commoderry@sanger.ac.uk commoderry@sanger.ac.uk on Jul 2, 2002 this sequence version replaced gi:21668136. AL807243.5 GI:21668234 HTG; HTGS_PHASE1; HTGS_DRAFT. 87572 GCCGAATCTATAAAAGGAA 87554

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                                                                                                                                                                                     Insert size: 184589; sum-of-contigs
Insert size: 18466; 5.5% error; agarose-fp
Quality coverage: 4.72x in Q2O bases; sum-of-contigs Quality
Coverage: 4.82x in Q2O bases, agarose fp
                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order is this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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3751 bp in length
100 bp
6905 bp in length
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4850 4949: gap of 100 bp
4950 22620: contig of 17671 bp in length
22621 22720: gap of "nn km"
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58284: contig of 2177 bp in length
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3524 bp in length
                                                                                      Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 175959 bases at least Q40
Consensus quality: 179463 bases at least Q30
Consensus quality: 182069 bases at least Q20
Center: Wellcome Trust Sanger Institute
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                                         Contact: humquery@sanger.ac.uk
                            Web site: http://www.sanger.ac.uk
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0: contig of 37
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2; Gaps
                                                              Query Match 76.4%; Score 106.2; DB 2; Length 186889; Best Local Similarity 89.4%; Pred. No. 6.1e-22; Matches 126; Conservative 0: Mismatches 13; Indels 2; 0
2348 others
52900 a 39593 c 40710 g 51338 t
  BASE COUNT
ORIGIN
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1; QY 1 GGGCCCGGCTCCACGTTTCTGCTGACTGACTACATAAACAGAGGCCGGGAA 60 HIII | Db 99260 GGGCCAIGTCTCCACGTGACTGAACTACATAAACAGAGGCCGGGAA 99201

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Search completed: February 4, 2003, 01:43:20 Job Lime: 748.962 secs

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February 3, 2003, 16:39:45; Search time 3108.84 Seconds (without alignments) 8559.21C Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugem Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                            using sw model
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	W748338 RC5-B	AA527406 ng37c02.s	AU135588 AU135588	AL698654 DKF2p686N	AC121731 AU121731	Z44377 HSC1Z3081 2
SUMMARIES	ID	10 AW748338	AA527406	AU135588	AL598654	AJ121731	14 244377
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ж	Query Match]	14.9	6.3	5.4	5.4	5.4	4.6
	Score	245.4	111.4	5.68	ග	თ დ	75
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34824 05981 8861 96898 56652	629 Dr 026 Dr 922 Te 613 Dr 460 Dr	54271 Drosophi 14204 AGENCOUR 31217 Pan trog 98882 Drosophi 7514 Drosophi	AGENCOUR Drosophi Brosophi Pan trog 7 60227087 7 60227087 7 60250phi 2 brosophi 2 brosophi 2 brosophi	35041 DTO 30617 Pan 30617 Pan 1325 ALS1 13475 Pan 43816 AGB 73529 Pan 50511 P93 03803 hv8	1031 Pan t
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ALIGNMENTS

Homo sapiens
Eukaryota, Netazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Amamalia; Eutheria; Primates; Catarrhini; Rominidae: Homo.
Theses 1 to 289;
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., adais,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J. EST 28-APR-2000 mRNA sequence. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, sequence tags Proc. Natl. Acad. Sci. J.S.A. 97 (7), 3491-3496 (2000) 289 bp mRNA linear RC6-ET0252-271099-012-c10 BT0252 Homo sapiens cDNA, AW748338 GI:7663270 EST. Contact: Simpson A.J.G. Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 human. DEFINITION ACCESSION ORGANISM RESULT 1 AW748339/c JOURNAL MEDIINE REFERENCE AUTHORS KEYWORDS VERSION TITLE COMMENT

source

FEATURES

BASE COUNT

Matches

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Clone distribution: NCI-CGAP clone distribution information can be
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/db_xref="taxon:9606"
                                                                                                   High quality sequence stop: 380.
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.8%;
Best Local Similarity 99.1%;
Matches 112; Conservative (
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                                                                                                                                                                                                                                                                                          /note="Vorgan: breast; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (0.5. Letters Patent application No. 196 7.76 - Ludwig Institute for Cancer Research) profiles into the pUC 19 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (۲)
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Oncublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, K.D., Michael R. Emmert-Buck, M.D.
             This sequence was derived from the FAPESS/LICR Human Cancer Genome Project. This entry can be seen in the following URL (Atter)/www.ludwig.org.Dr/scripts/gethtml2.pl?tl=RC6at2-RC6-BT0252-Seq primer: puc 18 forward
High quality sequence start: 146
High quality sequence stop: 289.

1. .289
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 6.3e-39;
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70 c 51 q
Email: asimpson@ludwig.org.br
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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SOURCE ORGANISM

KEYWORDS

VERSION

AUTHORS TITLE

JOURNAL

COMMENT

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RESULT 2 AA527406

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Chote Wester: PT7T3D-Pac (Pharmacia) with a modified Polylinker; Site 1: Not I; Site 2: Eco RI; Ist strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - Collog(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AU135588 AU135588 PLACZ1 Homo sapiens cDNA clone PLACE1002437 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0:
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HRI human cDMA project: 5'- s 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        816 TTIGTGGCCTCCTTCCTCTAATTTAIGAAGAAGCAGTAAGATGTTCCTCTCTCGGGTCC 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gabs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 111.4; DB 9; Length 467; Pred. No. 3e-12; 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 736)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         876 TCTGAGGGACCTGGGGAGCTCAGGCTGGGAATCTCCAAGGCAGTAGGTCGCCT
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helix Research Institute
1532-3 Yana, Kissrazu, Chiba 292-0812, Japan
                           www-bio.llal.gov/bbrp/image/;mage.html
Insert Length: 1057 Std Error: 0.00
Seq primer: -40mi3 fwd. ET from Amersham
                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:936962"
/clone_1ib="NoI_CGAP_CO3"
/sex="pooled"
```

SASE COUNT ORIGIN

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HRI human cDNA project
Unpublished (2000)
Condact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarau, Chiba 292-0812, Japan
Tel: 81-48-52-3976
Fax: 81-48-52-3976
Fax: 81-48-52-3976
Fax: 81-48-52-3976
Fix: B1-48-52-3976
Fix: B1-48-5
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                                                                                                                       EST 01-AUG-2002
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Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Honigatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Sebasilani-Kabaktchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi
Mammalia: Butheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 763)
Cta, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gabs
                                                                                                                    AU121731 AMMAN Homo sapiens cDNA clone MAMMAL000851 5', mRNA
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7.5e-08;
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/close_lib="MAMMAl"
/tissue_type="mammary gland"
/note="Vector: pMEH8SF13"
205 260 g 158 t
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/organism="Homo sapiens"
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Best Local Similarity 160.0°
Matches 89; Conservative
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                                                                                                                                                                               sequence.
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                                                             RESULT 5
AU121731
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KEYWORDS
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244377
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KEYWORDS
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                                                                                                                       LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKEZP686N12109_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone AL698654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenbuber, J. and Wiemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 547)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No s1 sequence available.
This clone (DKPZp685N12109) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GRRMANY; Email: clone@frzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1553 GTAATTGCGAGCGAGGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCTTCTCTC 1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Research Center (DKFZ); Email S.wiemann@dxfz- heldelberg.de; Sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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/tissue_type="human skeletal muscle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.4%; Score 89; DB 9; Le
100.0%; Pred. No. 8.5e-08;
tive 0; Mismatches 0;
                                                                                                                                                                            Score 89.4; DB 9;
Pred. No. 5.3e-08;
0; Mismatches 1;
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/clone_lib="PLACE1"
/tissue_type="placenta"
/note="Vector: pME18SFL3"
199 c 199 g 170
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/db_xref="taxon:9606"
/clone="DKF2p686N12109"
                                                                                                                                                                                                                                                                                                                                                                                                                                        51 CCGGCTGCGCAGGCGGGGGGGGGGCTC 91
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/lab_host="DH10B"
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154 c 157
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MIPS
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Sest Local Similarity 98.9%;
Matches 90; Conservative C
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Query Match

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CNS015W3
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                                                                                                                                                                                                                                                                                                                                                       /tissue_type="total brain"
/dev_stage="3 months old"
/dev_stage="3 months old"
/note="vorgan: brain, vector: lafmid BA; Site_1: EindIII;
Site_2: NoII; sex=Ferale; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total brain; total mnNA was oligo-(dn) primed and directionally cloned and directionally lafmid BA vector. Clone library from B.Soares, Psychiatry Dept. Columbia University, USA. Normalization_method:
Bento Soares, PN.A.S in press" 3 others
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (24-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Sethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                Email: cgapbs-remail.rih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G. E. Consortium (JLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                 Humain
Cedex, FRANCE
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and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 75; DB 14; Length 2>2
Pred. No. 6.7e-05;
                                                                                                                                                                                                                                                                                                                      /clone_lib="normalized infant brain cDNA" /sex="Female"
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                                                                                                Genethon Centre de recherche sur le Genome
1, rue de l'Internationale, BP60 91002 EVRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-12b08"
                                                                                                                                                                      genexpress@genethon.fr
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Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.68;
                                                            Contact: Genethon
Genexpress-Genethon
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Tel: 33169472800
Fax: 33160778698
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KEYWORDS
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Clone distribution: MGC clone distribution information can be found through the T.M.A.G.B. Consortium/Lint at: http://image.ilnl.gov Series: IRAK plate: 52 Rows of Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5915657 This clone has the following problem: incomplete processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web: www.genoscope.crs.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.cbi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CBPH (Centre of Etuce du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton pBelobACl1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                    X., Hulyk, S.W., Haie, S.M.,
S., Martin, R.G., Muzny, D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1569 GTGAGTGGGGCCGGGACCCGCAGAGCCSAGCCGACCCTTCTCTCTCCCGGGCTGCGGCAGGG 1628
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Drosophila melanogaster

Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha:

Ephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 1201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_rype="Skin, squamous cell carcinoma"
/clone_lib="NCI_CGAP_Skn4"
/lab_host="DH10b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1004;

    .1201
    /organism="Drosophila melanogaster"
/db_xref="taxon:7227"

Web site: http://www.hgsc.bom.tmc.edu/cdna/
Contact: amg@bom.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk
Yoon, V.S., Kowis, C.R., Lawrence, S., Martil
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMV-SPORI6.ccdb"
234 c 230 q 234 t
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100.0%; Pred. No. 4.3e-05;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="%omo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4749735"
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/clone_lib="DrosBAC"
/plasmid="pBeloBAC11."
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1571 GAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCA 1630
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GSS; genome survey sequence.
Tetracdon nigroviridis.
Tetracdon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                         Tetraodontidae, Tetr
I (bases 1 to 298)
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Best Local 8
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AUTHORS
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CNS04M2X
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://maqe.llnl.gov
Plate: LLAMIGGO3 row, column: 15
High quality sequence stop: 860.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              857 KRAAAMAMAAKMKTKAMTIGMARAIMKKDIGGGMAAIAAAGAAAAAWAWDDDADIIKKK
                                                                                                                                                                                                            917 TKTKGGKCSGGSCSGSCCTSCCSGSSSCARASMGGGSSSGGGGCCCMGGCCCGSGSCNGC
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Technologies. Note: this is a NCI_CGAP Library.
233 c 244 g 236 t
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 157 others
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                                                                               132;
                                             Score 60.8; DB 17;
Pred. No. 0.027;
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 232
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/db_xref="taxon:9606"
/clone="IMAGE:4749735"
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Technologies. Note.
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BASE COUNT
ORIGIN
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TITLE
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KEYWORDS

SOURCE

COMMENT

VERSION

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ORIGIN

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Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Terraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                           GSS 21-MAY-2000
l of clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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                                                                                                                                                                                                                                                                                                                                                                                                              Terraodon nigroviridis genome survey sequence T7 end of clone 119N17 of library G from Terraodon nigroviridis, genomic survey
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/db_xref="taxon:99883"
/clone="119N17"
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                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission

Sibmitted (00-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVAY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr - Web: www.genoscope.cns.fr - Web: www.genoscope.cns.fr - Web: www.genoscope.cns.fr - Getermination of this BAC-end sequence was carried out as part of collaboration with the Berkeley brosophila Genome Project (3DGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP brosophila melanogaster BAC library was prepared by Kazucoyo 30eogawa and Aaron Mammosor in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffallo, NY. The Library is named RP2CT-98 and was constructed by partial Goored Genetics at the Roswell Park Cancer Institute in Buffallo.

NY. The Library is named RP2CT-98 and was constructed by partial isogenic strain y2; or bw sp. the same strain used for the BDGP's place and BST libraries. A more detailed description of the library or fillers for hybridization from the BACPAC Resource Center can be found at http://bacpac.mec.buffalo.edu/drosophila_bac.htm.
                                                                                                                            Drosophila melanogaster genome survey sequence TET3 end of BAC # BACRIPH6 of RPCI-98 library from Drosophila melanogaster (fruit AL056652
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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/note="end : TET3"
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Drosophila melanogaster
1350 TCGTGGGCGGCTGAACGTCG 1379
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CNSOCGON 910 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14J21 of RPCI-99 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae:
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Uppublished (2001)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondal 2-1-2, Isukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7444
Fax: 81-298-88-7468
Email: tsasski@abr.afirc.go.jp, URL:http://rgp.dna.afirc.go.jp/
716 CTGTGTTTTTATCACAGGGAGGCTGATCAATAAATGAAATTAAAAGGGGGGTGGTCCCA 775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="hippombare"
/db xref="taxon:3947"
/clone="C10354"
/clone="Rice callus (2001)"
/tissue_type="callus"
24 c 102 t 4 others
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Rice cDNA from callus (2001)
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Similarity
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AL194922.1
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CNS02FE9/c
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Webb: www.genoscope.cns.if)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.ouffalo.edu/drosophila_bac.hum.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1238 TICCCGCGCGTCTTAGGCCGGGGGGGCGGGGGAAGGGGACGCAGACCGCGGACCT 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1118 AACTAACAAAGGAAAAAAAATIGCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGG 1177
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Neoptera: Endopterygota; Diptera: Brachycera: Muscomorpha;
Ephydroidea; Drosophilidae: Drosophila.
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  Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilae; Drosophila.
1 (bases 1 to 910)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        752 AASMARVAAVVARVASAAAVVASASAAVAVAAVSRSVASASRVMASAGSSASSSSSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            692 SASSSASSASMYVSCRSAVSVASAASAASARSASAVASAVAAVAASSSAVASSGSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          632 SCSSSRGGCSASSSSASASGSSSSSSSSSSSCGCGSCASSSSRSGSCGCGSSVGCVS
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/db_xref="taxon:7227"
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/clone_lib="RPCI-98"
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Matches 48; Conserv
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681 bp DNA linear GSS 13-MAY-2000 nigroviridis genome survey sequence PUC-Cri end of clone library G from Tetraodon nigroviridis, genomic survey
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                                                               Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP)-http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Ettude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Perraodontides; Petraodontides; Petraodon.

(tases 1 to 681)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Barnio, A., Pizames, C., Whocker, P., Brottier, P., Quetier, F., Barnio, W. and Weissenbach, J. Brottier, P., Quetier, F., Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
3P 191 91006 EVRY cedex - FRANCE (E-mail : segrefêgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Biliault, A., Quetler, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSS; genome survey sequence.
Tetracdon nigrovifidis.
Tetracdon nigrovifidis
Tetracdon nigrovifidis
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                /orgamism="Drosophila melanogaster"
/db_xref="taxon:7227"
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38.6%; Pred. No. 2.
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/plasmid="pBeloBAC1"
/note="end : T?"
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TITLE

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denoscope.
Direct Submission
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis scale. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                               /organism=""retracdon nigroviridis"
/db_xref="taxon:99883"
/clone="132:16"
/clone=lib="G"
/note="Genoscope sequence ID : COAG132BE08SP1-end
                                                                                                                                                                                                                                                                                                                                                                                                               Length 681;
                                                                                                                                                                                                                                                                                                                                                        125 others
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                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 3.1%, Score 51, D3 17, Le Best Local Similarity 31.5%, Pred. No. 3; Matches 88; Conservative 53; Mismatches 138;
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                                                                                                                                                                                                                                                                                                                                                        146 c
                                                    (bases 1 to 681)
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Nucleotide sequence of the 5' flanking region of the human ABC1 gene.
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Copyright (c) 1993 - 2603 Compugen Ltd.
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Adenosine triphosphate (ATP) binding cassette (A3C) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis

Claim 1; Page 143-144; 215pp; English.

The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (ATP) binding cassette protein (ABC) I gene. ABCI resides in cell membranes and utilises ATP indoloysis to transport a wide variety of substrates across the plasma membrane. ABCI is a priorial protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABCI is defective in Tanglar disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABCI gene is localised to chromosome 9422-9431. The ABCI genes and proteins are useful for developing pharmaceutical agents for the treatment of chert disease and other disorders associated with hypercholesterolemis and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indiadtors of cardiovaccular disease and cother disorders associated with hypercholesterolemia.

Sequence 1643 BP; 370 A; 413 C; 457 G; 403 T; 0 other;

0 420 480 120 180 246 300 300 360 420 540 Gaps 9 TCCTGTTGACTGTAGCAIGGAGGGGGCTTGTCAGCIGAATGTCTGTATGCAGGIGGTGGG AGTICTGGAATAIGATGGAGCTGGAGGTGGGAAGAGAAGTAGGCTTGGGGCAGCTCTCTC GCACITCCAGGGCCTGCTTGCTTCTACGGGTCTGTCCTGAGTCTTCTATGAATCTC CCTTCAGGGCAGATTCATATTTAGACTCTTCACAGTTTTGACCTGAGTTTTGGCCAGAATA AGGIGACATTTAGTTTGTTGGGTGGATGAGTGAGTTAAAATTTTAGACATATGGTGTGTAA CCCCTACACGCAAACGCAAACAGATAGTTGCAGGTCTGGAGTGGCTACATATTTAC TGTCCTGAGTGTTGATAGAACCACTGATGTGAGTACCTGGGCTTGAGCGTGGCCTGGAGA 241 ATGCCACCTCATTCTGGCCAAAACTCAGGTCAAACTGTGAAGAGTCTAAATGTGAATCTG GCACTTCCAGGGCCTGCTTGGCCTCTTCTACGGGTCTGTCCTGAGTCTTTTATGAATCTC CCCITCAAGGTGGCTACAAAGGTATCTTTGTCAAGGTAGGAGCCTTGTGGCCTCCACGT GOCCTECATTCCTACTCTTGCCTTTTTTTTTGCCCCTCCAGTGTTTTGGGTAGTTTTGCT :0 DB 22; Length 1643; 0; Indeis 100.0%; Score 1643; 100.0%; Pred. No. 0; live 0; Mismatches Conservative Similarity Best Local Sim Matches 1643; Query Match 121 541 181 481 9 61 121 181 241 301 301 361 361 427 421 481 541 001 Db qq QΫ́ QQ ŏά Op QQ ōγ qq δŏ qq $\stackrel{\wedge}{\circ}$ Op δ qq $Q\bar{Y}$ ΩŸ ŏλ õ

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AAF24703 standard; DNA; 1643

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1140 1200 1260 1320 1320 780 ACGACTGCAATTCTCTGGCTGCACTTCACAAATGTATACAAACTAAATACAAGTCCTGTG GCCGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGTG GACTAGAGAGICTGCGGCGCAGCCCCGAGCCCAGCGCTTCCCCGCGCGTCTTAGGCCGGGG TTTTTATCACAGGAGGCTGATCAATATAATGAAATTAAAAGGGGGCTGGTCCCATATTG AAACAAAAGCAGCCCATTACCCAGAGGACTGTCCGCCTTCCCCTCACCCCAGCCTAGGCC AAACAAAAAGCAGCCCATTACCCAGAGGACTGTCCGCCTTCCCCTCACCCCAGCCTAGGCC GECCCGGGCGGAAGGGGACGCAGACCGCGGACCCTAAGACACCTGCTGTACCCTCCA ATGAAGAAGCAGTAAGATGTTCCTCTCGGGTCCTCTGAGGGACCTGGGGGAGCTCAGGC TGGGAATCTCCAAGGCAGTAGGTCGCCTATCAAAATCAAAGTCCAGGTTTGTGGGGGGA CCGTTTAAGGGGCGCGGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTACAAAA COGTTTAAGGGGCCCCCGGCTCCACGIGCTTTCTGCTGAGTGACTGAACTACATAAA CAGAGGCCGGGAACGGGGGGGGGGGGAGGCACAGGCTTTGACCGATAGTAACCTC TGCGCTCGGTGCAGCGAATCTAAAAGGAACTAGTCCCGGCAAAAACCCCGGTAATTGC CGGCAGGCCAGGCGGGAGCTC 1643 CGGCAGGGCAGGGGGGGGCTC 1643 721 781 841 196 1021 1021 1081 1081 1142 1141 1201 1501 721 781 901 961 1201 1261 1261 1321 1321 1381 1381 1441 1501 1561 1561 1521 1521 õ QQ δ q ŏ OD ð CD ŏ qq $Q \underline{y}$ Db \tilde{Q} q ő g ${\bf Q}_{\underline{V}}$ QQ ΩŸ q $\delta \alpha$ Q δŏ qq οy qq á qq δŏ gg. ÓΫ g ŏ

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(first entry)
 20-APR-2001
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Human; adenosine triphosphate binding cassette protein 1; ABC1; apolitoprorein:mediated mobilisation; cholesterol; Tangler disease; chromosome 9422-9431; heart disease; hypercholesterolemia; ctherosclerosis; cholesterol transport; ss. the human ABC1 cf flanking region seguence of the 5'

Home

WO200078971-A2

16-JUN-2000; 28-DEC-2000

99US-0140264. 99US-0153872. 99US-0166573. 18-JUN-1999; 14-SEP-1999; 19-NOV-1999;

NC CV THERAPEUTICS UNIV WASHINGTON THERAPEUTICS (CVTH-) ((UNIW

Garvin Oram JF, Lawn RM, Wade D,

WPI; 2001-137811/14.

Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis

Disclosure, Page 138-139; 211pp; English.

The present sequence represents the 5' fianking region of the huumar adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the appolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.

Sequence 1643 BP; 370 A; 413 C; 457 G; 403 T; C other;

Query Match

0; TGTCCTGAGTGTTGATAGAACCACTGATGTGAGTACCTGGGCTTGAGCGTGGCCTGGAGA 120 9 1 GAATTCCTTGCTGGTGGCTCCACATGCACTTCCAGGGCCTGCTTGGCTCTTTCTATGGGTC DB 22; Length 1643; Indels . 0 100.0%; Score 1643; llarity 100.0%; Pred. No. 0; Conservative 0; Mismatches Similarity 1643; Matches 5 CC δŏ

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ICCTGTTGACTGTAGCATGGAGGGGGCTTGTCAGCTGAATGTCTGTATGCAGGTGGTGGG 180 121 20 g

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GACTAGAGAGTCTGCGGCGCAGCCCCGAGCCCAGCGCTTCCCGCGCGTCTTAGGCCGGCG 1260 420 720 780 840 241 ATGCCACCTCATTCTGGCCAAAACTCAGGTCAAACTGTGAAGAGTCTAAATGTGAATCTG 241 ATGCCACCTCATTCTGGCCAAACTCAGGTCAAACTGTGAAGAGTCTAAATGTGAAATCTG GCCCTGCATTCCTACTCTTGCCCTTTTTTTTGCCCCCTCCAGTGTTTTGGGGTAGTTTTGCT CCCCCTACAGCCAAAGGCAAACAGATAAGTTGGAGGTCTGGAGTGGCTACATAATTTTAC ACGACTGCAATTCTCTGGCTGCACTTCACAAATGTATACAAACTAAATACAAGTCCTGTG TTTTTATCACAGGGGGGGGTGATCAATATAATGAAATTAAAAGGGGGCTGGTCCCATATTG TGGGAATCTCCAAGGCAGTAGGTCGCCTATCAAAATCAAAGTCCAGGTTTGTGGGGGGA AAACAAAAGCAGCCCATTACCCAGAGGACTGTCCGCCTTCCCCTCACCCCAGCCTAGGCC AAACAAAAGCAGCCCATTACCCAGAGGACTGTCCGCCTTCCCCTCACCCAGCCTAGGCC ITTGAAAGGAAACAAAAGACAAAAAAAAATGATTGGCGTCCTGAGGGAGAITCAGCCTAG AGCTCTCTCTCCCCCATCCCTCCCTCCGGCTGAGAAACTAACAAAGGAAAAAAATT GOGGAAAGCAGGATTTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGTG GACTAGAGAGTCTGCGGCGCAGCCCCGAGCCCAGCGCTTCCCGGGGGTTCTTAGGCCGGCG GCCCCGGCGGGGAAGGGGACGCAGACCGCGGACCCTAAGACACCTGCTGCTCTCCA CCCTTCAAGGTGGCTACAAAGGTATCTTTGTCAAGGTAGGAGACCTTGTGGCCTCCACGT GCACTICCAGGGCCTGCTTGGCCTCTTCTACGGGTCTGTCTGAGTCTTCTATGAATCTC CCTTCAGGGCAGATTCATATTTAGACTCTTCACAGTTTTGACCTGAGTTTTGGCCAGAATA AGGTGACATTTAGTTTGGCTTGATGATGACTTAAATATTTAGACATATGGTGTGTA GGCCTGCATTCCTACTCTTGCCTTTTTTTTGCCCCTCCAGTGTTTTGGGTAGTTTTGGCT ATGAAGAGAAGCAGTAAGATGTTCCTCTCGGGGTCCTCTGAGGGACCTGGGGGAGCTCAGGC TITGAAAGGAAACAAAAGACAAGACAAATGATTGGCGTCCTGAGGGAGATTCAGCCTAG GCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGTG 541 1021 1081 1081 1141 361 421 181 481 601 721 781 841 901 961 961 1141 09 661 661 721 781 901 1201 021 1201 301 q g q δŏ Q Db Š Op QQ QC δď g δŏ G 20 a QΫ́ QQΫ́ ã g ŏ q ŎΣ 0,0 QY q Qγ qq δ g á 50 δ δğ

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Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;
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lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
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                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprottein-cholesterol (HDL-C) level, a higher than normal trigiveride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABCI expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected a
GGCCCGGGGCGGGGAAGGGGACGCAGACCGGGGACCCTAAGACACCTGCTGTACCCCTCCA 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds
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                                                                                                                               CCCCCACCCACCCACCTCCCCCAACTCCCTAGATGTGTCGTGGGCGGCTGAACGTCGC
                                                                    CAGAGGCCGGGAACGGGGGGGGGGGGGGGGGGGCACAGGCTTTGACCGATAGTAACCTC
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                                   CTTTGAAAGGAAACAAAAGACAAGACAAAATGATTGGCGTCCTGAGGGAGATTCAGCCTA
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AAAACAAAAGCAGCCCATTACCCAGAGGACTGTCCGCCTTCCCCCTCACCCGAGCCTAGGC
      TCCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGT
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Human, ATP-binding cassette 1, ABC1 gene regulation; atherosclerosis; choiesterol metabolism; hypercholesterolaemia; antisense therapy; ds.
                                                                    Human ABC1 transcription regulatory DNA #1.
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                AAD37265 standard; DNA; 3231
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                                                  (first entry)
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The invention relates a nucleic acid which is capable of regulating the transcription of human ATP-binding cassette 1 (ABC1) gene, which is a casual gene for pathologies linked to a dysfunctioning of cholotis a metabolism, including diseases such as atherosclerosis. Polynucleotides of the invention are used to screen candidate molecules or substances of that are capable of modulating the transcription of the ABC1 gene. They are used to artisense therapy. Compositions comprising sequences of the invention are used to treat inspercholesterolaemia and atherosclerosis. The present sequence is human ABC1 transcription regulating DNA.
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                                                                                 Isolated nucleic acid useful for modifying the ATP-binding cassette l (ABC1) and screening for candidate modulatory compounds or substances \,
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         Lemoine C, Naudis L, E
ev A, Santamarina-Fojo
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           Prades C,
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                                                                                Human ABC1 transcription regulatory DNA #3.
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CCIACTCTTGCCTTTTTTTTGCCCCTCCAGTGTTTTGGGTAGTTTTGCTCCCCCTACAG
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                                 GGCTACAAAGGTATCTTTGTCAAGGTAGGAGACCTTGTGGCCTCCACGTGCACTTCCAGG
                                                                             GCCTGCTT-GGCCTCTTCTACGGGTCTGTCTGAGTCTTCTATGAATCTCCCTTCAGGGC
                                                                                                                          AGATTCATATTTAGACTCTTCACAGTTTGACCTGAGTTTTGGCCAGAATAAGGTGACATT
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The invention relates to an isolated human large ATP-binding cassette transporter 1 (ABC1) promoter capable of directing transcription of neterologous coding sequence positioned downstream to it. The hABC1 promoter is useful for expressing foreign DNA in a host cell, by introducing into the host cell a gene transfer vector comprising the promoter operably linked to a foreign DNA encoding a desired polypeptide or RNA, where the foreign DNA is expressed. The gene transfer can be introduced into the host cell by adecovirus infection, liposome-mediated transfer, topical application to the cell or microlnjection. The gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transfer vector encodes and expresses a resorter molecule. The method further involves introducing into the cell a gene transfer vector comprising a nucleic acid segment encoding a transactivator protein capable of upregulating the ABCI promoter, or contacting the cell with the transactivator protein, or an agonist of the transactivator protein, or an agonist of the transactivator protein Modulators of human ABCI gene expression are useful for treating atherosclerosis. The present sequence represents the MABCI promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human large ATP-binding cassette transporter 1(hABC1) promoter sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated human large ATP-binding cassette transporter 1 promoter capable of directing transcription of heterologous coding sequence positioned downstream to it, useful for expressing foreign DNA in bost
                               TAAACAGAGCCGGGAACGGGGGGGGGGAGGGAGGGAAGCACAGGCTTTGACCGATAGTAA 1496
                                                                                                                                                                                        CCTCTGCGCTCGGTGCAGCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCGTAA 1556
                                                   Human, large ATP-binding cassette transporter 1, ABC1, promoter; antiarteriosclerotic, gene transfer, transactivator; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1197 BP; 284 A; 314 C; 328 G; 271 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                   DNA; 1197
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                  Gaps
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                                                                                                                                              640 GGAGIGGCIACATAATITIACACGACIGCAAITCICIGGCIGCACIICACAAAIGIAAA
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                                                                                                                                                        240 AAACTAAATACAAGTCCTGTGTTTTATCACAGGGGGGGTGATCATAATGAAATTAA
                                                                                                                                                                                                                                                           TGGCCTCCTTCCTCTATTTATGAAGAAGCAGTAAGATGTTCCTCTCGGGTCCTCTG
                                                                                                          AAACTAAATACAAGTCCTGTGTTTTTAICACAGGGAGGCTGATCAATATAATGAAATTAA
                                   460 ACCICAGITITGGCCAGAATAAGGTGACATTTAGITTGTTGGCTTGATGAATGACTTAAA
                                                Length 1197
                  3,
                  Indels
 DB 24;
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Score 1146.4; DB 24
Pred. No. 1.2e-306;
); Mismatches 1;
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 69.8%;
99.7%;
                     Conservative
            Similarity
                     Matches 1180;
   Query Match
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The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from identified within the present sequence. The 5' ESTS were prepared from forth hann RNAs or polyA+ RNAS derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from olige'dT primed cDNA ilbraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTS are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                      5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGCAAAAACCCCGTAATTGCGAGCGAGAGTGAGTGGGGCCGGGGACCCGCAGAGCCGAGC 1599
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid that is a 5' expressed sequence tag (5' EST) for aining cDNAs and genomic DNAs that correspond to 5'ESTs and for nostic, forensic, gene therapy and chromosome mapping procedures
GCTITGACCGATAGTAACCTCIGCGCTCGGTGCAGCCGAATCIATAAAAGGAACTAGTCC
               1018 GCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAATCTATAAAGGAACTAGTCC
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                                                                                                                                   CGACCCTTCTCTCCCGGGCTGCGGCAGGCCGGGGGGGGCTC 1643
                                                                                                                                                          Similarity 99.2%; Pred. No. 7.1e-23; 0: Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostic, forensic, gene therapy and chromosome
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                                                                                                                                                                                                                                                                                                                                                    Human secreted protein 5' EST, SEQ ID NO: 13690.
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                                                                                                                                                                                                                                                           AAC09615 standard; cDNA; 227
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bcund_moiety= "LMO2-COM/MYOD/deltaEF1/647"
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//bound_moiety= "MZF1"
//bound_moiety= "IK2/NFkappaB/CREL"
/*tag= ao
/bound_moiety= "IK2/NFkappaB/CREL"
2259..2272
                                                                                                                             "DeltaEF1/LYF1/1K2"
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Thound_moiety= "PPAR/NKX2.5/PPAR"
$C19..2024
*ttag= aj
Thound_moiety= "PPAR/NKX2.5/PPAR"
                                                                                            "LXRalpha/deltaEF1"
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1221..2228
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/bound_moiety= "HNF3beta"
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2008..2016
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bound_moiety= "DeltaEF1"
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bound_moiety= "SOX5"
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bound_moiety= "AP1"
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1809..1819
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1173..1188
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2104..2111
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597..1607
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189..1209
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Human, AFP-binding cassette 1; ABC1 gene regulation, atherosclerosis, cholesterol metabolism; hypercholesterolaemia; antisense therapy; ds.
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bound_moiety= "LMO2COM/MYOD/DeltaEF1"
649..556
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bound_moiety= "HFH2/SRY/EVI1"
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/*tag= p
/bound_molety= "CREBP1/VBP"
                                                                                                                                                                                                        Human ABC1 transcription regulatory DNA #3.
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/bound_moiety= "S3/NKX2.5"
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'Dound_moiety= "DeltaEF1"
.10..125
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/bound_moiety= "NFY/CAAT"
708..715
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/bound_moiety= "LXX2.5"
608..620
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'bound_moiety= "MZF1"
'71...785
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'Cound_moiety= "MZF1"
'23..730
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'bound_moiety= "GATA"
899..410
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/bound_moiety= "LYF1"
528..539
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bound_moiety= "lYF1"
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412..420
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AAD37267/c
ID AAD37267 standard; DNA; 2910 BP.
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1700 GAAGIGCACGIGGAGGC--CACAAGGICICCIACCITGACAAAGAIACCIITGTAGCCAC 1643
                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid useful for modifying the ATP-binding cassette 1 (ABC1) and screening for candidate modulatory compounds or substances \,
                                                                 1760 CCCTGAAGGATTCATAGAAGACTCAGGACAGACCCGTAGAAGAGGCCCAAGCAGGCCCTG 1701
                                                                                                                                                                                                                              Human; ATP-binding cassette 1; ABCl gene regulation; atherosclerosis; cholesterol metabolism: hypercholesterolaemia; antisense therapy; ds.
CCCTTCAAGGTGGCTACAAAGGTATCTTTGTCAAGGTAGGAGACCTTGTGGCCCTCCACGT
                                 GCACTICCAGGGCCIGCIIGGCCICTTCTACGGGICIGICCIGAGICITCIATGAAICIC
                                                                                                                                                                                                               Human ABC1 transcription regulatory DNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 130-131; 152pp; English.
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Prower R. Duverger N, Remaley A,
                                                                                                                                                               AAD37265 standard; DNA; 3231
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*tag= ap
/bcnd_moiety= "LMO2COM/GATA"
2289..2306
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                                "MZF1/SRY
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bound_moiety= "RREB1"
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8442..2451
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2361..2384
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                                                         "PPAR"
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bound_moiety= "SRY"
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/bound_moiety= ";
2610..2617
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2728..2740
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Denefle 1

s C, Naudin L, D Santamarina-Fojo

Lemoine C,

The invention relates a nucleic acid which is capable of regulating the transcription of human ATP-binding cassette 1 (ABC1) gene, which is a casual gene for pathologies linked to a dysfunctioning of cholesterol metabolism, including diseases such as atherosclerosis. Polynucheotides of the invention are used to screen candidate molecules or substances that are capable of modulating the transcription of the ABC1 gene. They are used to antisense therapy. Compositions comprising sequences of the invention are used to treat hypercholesterolaemia and atherosclerosis. The present sequence is human ABC1 transcription regulating DNA. ATECCACCICATTCIGGCCAAAACTCAGGTCAAACTGTGAAGAGTCTAAATGTGAATCTG 300 Gaps DB 24; Length 3231; 2; 83; Indels Sequence 3231 BP; 809 A; 773 C; 876 G; 773 T; 0 other; Score 102.2; DB 2 Pred. No. 1.6e-17; 0; Mismatches 65.28; Conservative Similarity Query Match Best Local Simi Matches 164; 241 gc 92

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Gaps

83:

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241 AIGCCACCICATICIGGCCAAAACICAGGICAAACIGIGAAGAGICIAAAIGIGAAICIG 300

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1546 AAACCCCCTAATTSUGAGCGAGAGTGAGTGGGGGCCGGGACCCGCAGAGCCGAGCCGACCC 1605
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/note= "alternative open reading frame of AAI70314"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of cDNA encoding the human adenosine triphosphate (APP) binding cassette transporter 1 (ABC1) protein (see AAMS0227). The sequence includes an extended open reading frame (ORF) to that provided by the sequence in AAI70314, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP binding cassette transporter 1; ABC1; human; lipid disorder; cholesterol; cardiovascular disease; inflammatory disease; antiinflammatory; antilipaemic; antipsoriatic; dermatological; Tangler disease; coronary heart disease; diagnosis; gene therapy;
Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ATP binding cassette transporter 1 (ABC1) cDNA.
                                                                                                                                                                                                               1606 TTCTCTCCCGGGCTGCGGCAGGGCAGGCGGGGGAGCTC 1643
                                                                                                                                                                                                                                     61 TICTCTCCCGGGCTGCGCAGGCAGGCCGGGAGCTC 98
                                                                   Pred. No. 3.4
Mismatches
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                                             6.0%; Score 98;
100.0%; Pred. No.
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replace(3836,C)
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                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; AIP binding cassette transporter 1; ABC1; coronary heart disease; dermatological; atherosclerosis; cardiovascular; inflammatory disease, psoriasis; lipid disorder; antibacterial; septic shock; gene therapy; immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                       1642 CTTGAAGGCCAGATTCACATTTACACTCTTCACAGTTTGACCTGAGTTTTTGCCAGATG 1583
                                                                                                                                                        1700 GAAGIGCACCIGGAGGC - CACAAGGICTCCIACCIIGACAAAGAIACCIITGIAGCCAC 1643
                                                               CCTTCAGGGCAGAITCAIATTIAGACICTTCACAGITTGACCTGAGITTIGGCCAGAATA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New adenosine triphosphate binding cassette transporter-1 gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                     CCCITCAAGGTGGCTACAAAGGTAICTTTGTCAAGGTAGGAGACCTTGIGGCCTCCACGT
                                                                                                                     361 GCACTTCCAGGGCCTGCTTGGCCTCTTCTACGGGTCTGTCCTGAGTCTTCTATGAATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ATP binding cassette transporter 1 (ABC1) gene.
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321..7106
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                                                                                                                                                                                                                                                                                                                                1582 AGGTGGCAT 1574
                                                                                                                                                                                                                                                                                           481 AGGTGACAT 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAE13022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JAN-2002
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RESULT 10 AAD21326

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1546 AAACCCCGTAATTECGAGCGAGCGAGTGAGTGGGGCCGGGACCCGAGAGCCGAGCCGACCC 1605
an alternative ATG codon as initiation codon and thereby adding acceptant 40 N-terminal amino acids to the encoded ABCI protein (see AAMS022B). The invention provides 4 common polymorphisms in the ABCI gene. These were identified by sequencing the ABCI gene in different Tangier kindreds. In the variant genes (numbering as in AAT70314), G is changed to A at position 596, T is changed to C at position 1136, A is changed to G at position 596, T is changed to C at position 1136, A is changed to G at position 596, T is changed to C at position 136, A is changed to G at position 596, T is changed to C at position 136, A is changed to G at position 596, T is changed to C at position 136, A is changed to G at position 596, T is changed to C at position of these. All of therefore may affect its function. The 2 most common polymorphisms (6596A) and A258G) are both associated with a decreased in vitro ApoA-I conducted efflux of cholesterol from monounclear phagocytes, a feature typical of Tanglez disease. 3 of the variants (656A, A258GG and 63456C) are significantly increased in a population of estabished coronary heart disease (CHB) relative to CED-free control subjects. The use of the provided ABCI polymorphisms for the diseases, and inflammatory diseases (CHB) relative to CED-free crythematodes) is claimed Modulation of ABCI transcripts of the provided ABCI transcripts of the provided ABCI transcripts of the action of ABCI transcripts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of the 5' flanking region of the human ABCl gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; choiesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia;
                                                                                                                                                                                                                                                                                                                                                                                                                 2150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                          erythematodes) is claimed. Modulation of ABC1 transcripts or proteins by antisense or ribozyme technology or RNA Gecoys is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leagth 7260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.0%; Score 98: DB 22; I Local Similarity 160.0%; Pred. No. 3.4e-16; es 98; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trererecessergesseassessessessesses 1643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atherosclerosis; cholesterol transport; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF24681 standard; DNA; 1643 BP
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19-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         claimed.
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The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (ATP) binding casette protein (ABC) I gene. ABCI resides in cell membranes and utilises ATP indcloysis to transport a wide variety of substrates across the plasma membrane. ABCI is a pivotal protein in the apolipoprotein mediated mobilisation of intracellular protein in the apolipoprotein mediated mobilisation of intracellular choisterol stores. ABCI is defective in Tanglar disease. A genetic choiseterol stores abcorned HDL-choisterol metabolism. The ABCI gene is localised to chromosome 9422-9431. The ABCI genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with care also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hyperchoiesterolemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 IGGAAGIGCACGIGGAGGCCACAAGGTCTCCITACCTIGACAAAGATACCTTIGTAGCCAC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ATGCCACCTCATTCTGGCCAAAACTCAGGTCAAACTGTGAAGAGTCTAAATGTGAATCTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCTICAAGGIGGCIACAAAGGIAICITIGICAAGGIAGGAGACCIIGIGGCCICCACGI 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCITCAGGGCAGATICATATITAGACICTICACAGITITGACCIGAGITITGGCCAGAATA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of the 5' flanking region of the human ABC1 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              5.9%, Score 97, DB 22; Length 1643; 61.8%, Pred. No. 3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95; Indels
and other disorders associated with hypercholesterolemia
                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 1643 BP; 370 A; 413 C; 457 G; 403 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                          Claim 1; Page 143-144; 215pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 154; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 AGGIGGCAT 241
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                          atheroscierosis
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19-NOV-1995;

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27714 ATGTCACCITATICTGGCCAAACTCAGGTCAAACTGTGAAGAGTCTAAATATGAATCTG 27655
                                                                                                                                                                                                                                                                                                                                                                                                            Treating a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardicvascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABCl expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;
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Pred. No. 5.3e-14;
0; Mismatches 90;
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                                                                                                                                                                                                                                                                                                                      Brooks-Wilson AR,
                                                                                                                                                                                                                                         (UYBR-) UNIV BRITISH COLUMBIA
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23-JUN-2000; 2000US-0213958.
                                                                                             01-SEP-2000; 2000WO-IB01492
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                                                                                                                                                                                                                                                                     (XENO-) XENON GENETICS INC.
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WO200115676-A2
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                                              08-MAR-2001
                                                                                                                                                                                                                                                                                                                      Hayden MR,
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                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (ATP) binding cassette protein (ABC) I gene. ABCI resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABCI is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABCI is defective in Tangler disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABCI gene is localised to chromosome 9q22-9q31. The ABCI genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and
                                                                                                                                                                                                                    Agenosine triphosphate (AIP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High density lipoprocein-cholesterol; HDL-C; cardiovascular; ABCl; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 CITGAAGGGCAGAITCACATITAAGACICITCACAGTITGACCIGAGTITIGAGGCAGAATG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 TGGAAGTGCACGTGGAGGCCACAAGGICTCCTACCTTGACAAAGATACCTTTGTAGCCAC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 CCTTCAGGGCAGATTCATATTTAGACTCTTCACAGTTTGACCTGAGTTTTGGCCCAGAATA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 ATGCCACCTCATTCTGGCCAAAACTCAGGTCAAACTGTGAAGAGTCTAAATGTGAATCTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are also useful as diagnostic indicators of cardiovas
other disorders associated with hypercholesterolemia.
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                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 138-139; 211pp; English.
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Pred. No.
                                                                                                                            Garvin M;
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AAF92831 standard; DNA; 183999 BP.
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       99US-0166573
                                                      CV TEERAPEUTICS INC
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Matches 154; Conservative
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                                                      (CVTH-) CV THERAPEUTICS (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                             WP:: 2001-137811/14.
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Query Match

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Gaps

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17-MAY-2001

AAF92831;

RESULT 14 AAF92831

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The invention relates a nucleic acid which is capable of regulating the transcription of human ATP-binding cassette 1 (ABC1) gene, which is a casual gene for pathologies linked to a dysfunctioning of cholesterol metabolism, including diseases such as atherosclerosis. Polynucleotides of the invention are used to screen candidate molecules or substances that are capable of modulating the transcription of the ABC1 gene. They are used in antisense therapy. Compositions comprising sequences of the invention are used to treat hypercholesterolaemia and atherosclerosis. The present sequence is human ABC1 gene exon 1A.
                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid useful for modifying the ATP-binding cassette l (ABCI) and screening for candidate modulatory compounds or substances \,
cholesterol metabolism; hypercholesterolaemia; antisense therapy;
                                                                                                                                                                                                                                                                          Rosier-Kontus M, Prades C, Lemoine C, Naudin L, Denefle P;
Brewer B, Duverger N, Remaley A, Santamarina-Fojo S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 5.1e-15;
Matches 91; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 132; 152pp; English.
                                                                                                                                                                     02-MAY-2001; 2001WO-EP05488.
                                                                                                                                                                                                          02-MAY-2000; 2000US-201280P.
                                                                                                                                                                                                                                             (AVET ) AVENTIS PHARMA SA.
                                                                                                                                                                                                                                                                                                                                        WPI; 2002-154404/20.
                                                                                               WO200183746-AZ.
                                                            Home sapiens
                                                                                                                                    08-NOV-2001.
                           exon 1A; ds.
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Search completed: February 3, 2003, 16:20:03 Job time : 972.868 secs

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0; Gaps

1553 GTAAITGOGAGCGAGAGTGAGTGGGGGCCGGGACCCGCAGAGCCGAGCCGACCCITCTCTC 1612

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1613 CCGGGCTGCGGCAGGGCGGGGGGGAGCTC 1643

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61 CCGGGCTGCGGCAGGCCGGGGGGGCTC 91

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US-08-232-463-14
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STATE:
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6534.066 Million cell updates/sec
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                                                                                             3, 2003, 12:56:40 ; Search time 16.5211 Seconds
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Sequence 1,
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Sequence 5,
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COM5.seq:*
/cgn2_6/ptodata/1/ina/6B_COM5.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COM8.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COM8.seq:*
                           Compugen Ltd.
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US-09-276-531-56
US-09-7122-1268-14
US-09-485-549-1
US-08-870-18-8
US-08-870-18-8
US-09-750-580-1
US-08-672-1098-9
US-08-672-1098-9
US-08-842-045-9
US-08-842-045-9
US-08-842-045-9
US-08-842-045-9
US-08-842-045-9
US-08-93-358-9
US-08-672-1098-9
US-08-69-3358-9
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US-08-69-3358-9
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US-09-098-628-1
US-09-098-628-1
US-08-651-136C-7
US-08-651-136C-7
US-08-651-136C-7
US-08-469-318-7
US-08-469-318-7
US-08-469-318-7
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          GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compug
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US-08-458-609A-71
                                                                                                                                                    US-39-596-141C-3_COPY_1292_1643
                                                                                                                                                                                                                                                    441362 seqs, 153338381 residues
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                                                                                                                                                                                                                                                                                                                                                                     Maximum Match 100%
Listing first 45 summaries
                                                                  nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATICN:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEGGENCES: 52
US-08-446-872A-68
US-08-446-872A-70
US-08-762-227A-70
US-08-762-227A-70
US-08-762-227A-71
PCT-US95-01185-68
PCT-US95-01185-70
PCT-US95-01185-70
US-08-306-691B-19
US-08-83-06251-19
US-08-87-11
US-08-87-11
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US-09-109-204-6
US-09-335-409-1
US-09-568-102-1
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                                                                                                                                                                                                                                              ALIGNMENTS
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APPLICATION NUMBER: BP 91 114 360.6
FILING DATE: 26-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/37/935,313
                                                                                                                                                                                                                                                                                            5-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: SENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFRENCE/DOCKEI NUMBER: 3047;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9303
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : Floppy disk
IBM PC compatible
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INFORMATION FOR SEC ID NO:
SEQUENCE CHARACTERISTICS:
  nucleic ació
EDNESS: single
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ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
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OPERATING SYSTEM:
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  STRANDEDNESS:
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Length 7218;

DB 1;

Score 35;

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APPLICANT: BEASLEY, Ellen M. et al TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING EUMAN KINASE PROTEINS, AND USES FILE OF INVENTION: THEREOF FILE PEFERENCE: CLOO1061
                                                                                                                  1157 recercaacrecriegegeregesagegacrecrecrecerran---ecergee 1213
                                                                                                                                                                              1214 TGGGTATTCCCTACCTTTCTGGTCTCTGAGACTTACCTCTTCCAGAAGTCCTCCGGA 1273
                                                                              107 CCCGGCTCCACGTGCTTTCTGCTGAGTGACTACATAAACAGAGGCCGGGAACGGG 166
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     Length 1610;
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                                                                                                                                                                                                                                                         1274 ATGAGTAGAAGGGAGGTGGATTGGAACTTAAGIGACATCTGG 1320
                                           73; Indels
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                                                                                                                                                                                                                                  167 GCGGGGAGGAGGAGCACAGGCITTGACCGATAGTAACCTCTGCG 213
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
FILE REFERENCE: DM699
CURRENI APPLICATION NUMBER: US/09/122,126B
CURRENI FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
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63.3%; Pred. No. 2.9;
         DB 4;
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     Score 34,2; DB Pred. No. 0.85;
                                           0; Mismatches
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Pred. No. 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/741,154 CURRENT FILING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                                                                          US-09-122-126B-14/c; Sequence 14, Application US/09122126B; Patent No. 6451575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09741154
Patent No. 6437110
GENERAL INFORMATION:
     9.78;
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                                           91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (121)..(2910)
US-09-122-126B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 16389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 14
LENGTH: 3250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-741-154-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-741-154-3
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                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reddy, Roopa
APPLICANT: Reddy, Roopa
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TILLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
TILLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
NUMBER OF SEQUENCES: 134
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                                                                                                                                                                                                                                    190 CTITGACCGATAGIAACCTCTGCGCTCGGTGCAGCCGAATCIATAAAAGGAACTAGTCCC 249
                                                     250 GGCAAAAACCCCGTAATTGCGAGCGAGAGTGAGTGGGGCCCGGGACCCGCAGAGCCGAGCC 309
                     ..
                     Indels
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APPLICATION NUMBER: US/09/276,531
FILING DATE: Herewith
                   83;
8.0%; Pred. No. 0.76;
cive 113; Mismatches
                                                                                                                                                                                                                                                                                                                  1065 redealecrecerdacerdecadered 1033
                                                                                                                                                                                                                                                                               310 GACCCTTCTCTCCGGGCTGCGGCAGGGCAGGG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HINCYTE PHARMACEUTICALS, INC. 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PA-0008 US
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Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 56, Application US/09276531 Patent No. 6183968 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60/079,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: March 27, 1998 CLASSITICATION:
ATTORNEY/AGENT INFORMATION:
ARME: Lyon E. Murry, Ph.D. REGISTRATION NUMBER: 42,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/079,(FILING DATE: March 27, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lal, Preeti
APPLICANT: Fillman, Jennifer
APPLICANT: Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (650) 855-0555
(650) 845-4166
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H: 1610 base pairs
nucleic acid
DEDNESS: single
Best Local Similarity 8.0%, Matches 17; Conservative
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SEQUENCE CHARACTERISTICS:
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; CLONE: 1396833
US-09-276-531-56
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CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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US-09-276-531-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1359 CAGGIGGGCCTGGGICACAGCAGGTTGATCTCGTCCAGGIAGCGGGGGGGAGCACCGAGTC 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 GGGGGGCCCCGGCTCCACGTGCTTCTGCTGAGTGACTGAACTACATAAACAGAGGCCGG 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANDISENSE MODULATION OF G-ALPHA-16 EXPRESSION
TITLE OF INVENTION: ANDISENSE
CURRENT REFERENCE: RTG-003
CURRENT APPLICATION NUMBER: US/09/205,143
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: Fast530 for Windows Version 2.0
CURRENI APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31.4; DB
Pred. No. 5.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31.4; D. Pred. No. 5.7; 0; Mismatches
                                                                                                                                                                                                                                                                       04020/102001
                                                                                                                       APPLICATION NUMBER: US/08/870,518
FILING DATE: 06-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/019,219
FILING DATE: 06-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/09205143
; Patent No. 6107091
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 GAACGGGGCGGGGAGGGA 180
                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                      32,983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 cecceecceecceecca 83
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61.78;
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                                                                                                                                                                                                                                                                                                                                                                                              1817 base pairs
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Best Local Similarity 61.7'
Matches 50; Conservative
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Best Local Similarity 53.77
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ 1D NO:
                                                                                                                                                                                                                                   NAME: Fasse, Peter J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                          617/542-50
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                     single
   ZIP: 02110-2834
COMPUTER READABLE FORM:
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US-09-205-143-1
                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                       TELEPHONE: 617,
TELEFAX: 617/5
TELEX: 200154
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                            APPLICANT: James Tricoli
APPLICANT: Rachel Rhondinelli
APPLICANT: Fox chase Cancer Center
APPLICANT: Fox Chase Cancer Center
IITLE OF INVENTION: prognostic Compositions for Prostate Cancer and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ġ.
                                                                                                                         12771 GCGTCTCCTGGGGGTGAATCCTGCACCAGGGCTGTACATTGTCATGGAGCACGTGACCAA 12830
                                                                 12711 CCAGCCTCCCTCACGCCCACCCCCCCCCAGGAAGATGCAACAAGAACGTGGT 12773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 AGGGCGGGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAACAGAGGC 156
 Gaps
                                 30 CCCCACCCACCACCACCACCCCCAACTCCCTAGATGTGTCGTGGGCGGCTGAACGICGC 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 CCCACCCACCTCCCCCAACTCCCTAGATGTGTCGTGGGGGGGCGCTGAACGTCGCCCGTTTA 96
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 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Davis, Roger J.
APPLICANT: Galcheva-Gargova, Zoya
TITLE OF INVENTION: NON-ACTIVATED RECEPIOR COMPLEX
TITLE OF INVENTION: PROFEINS AND USES THEREOF
 73;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/055,285
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SEQ ID NO:
                                                                                                                                                                                                12831 GGTGGGGGGGGCCCAGGGGGGGGGG 12859
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: FCCC 95-13
CURRENT APPLICATION NUMBER: US/C9/485,549
CURRENT FILING DATE: 2000-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT/US98/16768
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                                                                                                                                                                         150 CAGAGGCCGGGAACGGGGCGGGGAGGAGG 178
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1998-08-13
THEP: 60/055,285
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225 Franklin Street
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                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09485549
Patent No. 6361949 GRNSRAL INFORMATION:
APPLICANT: James Tricoli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08870518
Patent No. 5925565
GENERAL INFORMATION:
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Conservative
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PRIOR FILING DATE: 1998-0
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 82; Conserv
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STREET: AL.
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JID NO I
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US-08-870-518-8/c
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76;
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                                                                                                                                                                                                                                                             RESULT 5
US-09-485-549-1
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Matches
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LOCATION: 45442
OTHER INFORMATION: 20-842-115 : polymorphic base A or G NAME/KEY: allele
LOCATION: 77058
                                                                                         : polymorphic base C or I
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LOCATION: 1240..1256
OTHER INFORMATION: 20-828-311.mis complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 45423.45441
OTHER INPORMATION: 20-842-115.mis
LOCATION: 45443.45461
OTHER INPORMATION: 20-842-115.mis complement
MAMP/KEY: primer_bind
LOCATION: 77039..77057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 20-841-149.mis complement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 12348. 12366
OTHER INFORMATION: 17-42-319.mis complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: 20-841.rp complement NAME/KEY: primer_bind_CCATION: 45828..45347
OTHER INFORMATION: 20-842.pu
NAME/KEY: primer_bind
LOCATION: 45863..45883
OTHER INFORMATION: 20-842.rp complement NAME/KEY: primer_bind
                                                                                                                                                                                                                OTHER INFORMATION: 20-828.rp complement
NAME/KEY: primer_bind
LOCATION: 12029..12050
LOCATION: 17-42.pu
NAME/KEY: primer_bind
LOCATION: 12581..12603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement
                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 17-42.rp complement NAME/KEY: primer_bind LOCATION: 14952..15010
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 15460. 15482
OTHER INFORMATION: 17-41.rp complement
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OTHER INFORMATION: 17-42-319.mis
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LOCATION: 15222..15240
OTHER INFORMATION: 17-41-256.mis
                                                                            OTHER INFORMATION: 20-853-415
NAME/KEY: primer_bind
LOCATION: 929..949
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OTHER INFORMATION: 20-853.rp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: primer_bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer_bind
LOCATION: 42572..42591
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NAME/KEY: primer_bind
LOCATION: 77166..77185
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OTHER INFORMATION: 20-828.pu
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OTHER INFORMATION: 17-41.pu
NAME/KEY: primer_bind
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LOCATION: 15242..15260
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LOCATION: 1220..1238
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LOCATION: 45423.,4544
                                                                                                                                                                                                                                                                                                                 APPLICANT: DOLLERL, Aymeric
APPLICANT: Bougueleret, Lydie
APPLICANT: Ebbets-Reed, Dana
APPLICANT: Salter-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 42218
OTHER INFORMATION: 20-841-149 : polymorphic base A or G
NAME/KEY: allele
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                                                                                                                                                                                                                                                         Bour, Barbara
Bihain, Bernard
Dumas Milne Edwards, Jean-Baptiste
                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 89.082.CIP
CURRENT APPLICATION NUMBER: US/09/750,580
CURRENT FILING DATE: 2300-12-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2003-06-21
PRIOR APPLICATION NUMBER: PCT/IB99/02058
PRIOR FILING DATE: 1999-12-20
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UMBER: US 50/141,032
1999-06-25
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OTHER INFORMATION: 5'regulatory region
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                                                                                                       RESULT 8
US-09-750-580-1/c
Sequence 1, Application US/09750580
Patent No. 6455280
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PRIOR APPLICATION NUMBER: 1
PRIOR FILING DATE: 1999-12
PRIOR APPLICATION NUMBER: 1
PRIOR FILING DATE: 1998-12
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LCCATION: 12947..12958
OTHER INFORMATION: exon 1
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LOCATION: 13470..13526
OTHER INFORMATION: exon 2
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PRIOR FILING DATE: 1999-0
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OTHER INFORMATION: excn 3
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NAME/KEY: misc_feature
LOCATION: 15969..17969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ICATION NUMBER:
                                                                                                                                                                                                                   Yen, Frances
Denison, Bla
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LOCATION: 10946.12946
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SEQ ID NO 1
LENGTH: 81001
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PRIOR FILING DATE:
                                                                                                                                                                                          GENERAL INFORMATION:
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LOCATION: 12347
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1299 C 1299
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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ATTOORBY/AGENT INDORMATION:
NAME: Smith, Deann F
RECISTRATION UMBER: 36683
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MOLECULE TYPE: DNA (genomic)
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APPLICANT: Gantz, ira
IITLE OF INVENTION: Genes E:
                                                                                                                                                                                                                   Query Match 8.9%;
Best Local Similarity 47.1%;
Matches 96; Conservative
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CITY: Bloomfield Hills
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LENGTH: 975 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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         double
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ADDRESSE: Harness,
STREET: P.C. 30x 828
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FILING DATE: June 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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SOFIWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5710265
GENERAL INFORMATION:
                                                                                                              Mouse
         STRANDEDNESS:
                                                                           0N
                                                                         ANTI-SENSE: NO
ORIGINAL SOURCE
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                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                            ORGANISM:
                                                                                                                                                                                  US-08-671-525B-9
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                                                                                                                              FEATURE:
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COMPLIEN.
CORREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/671,525B
FILING DATE: June 27, 1996
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STREET: P.O. Box 828
CITY: Bloomfield Hills
                                  LOCATION: 77059.77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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Pred. No. 15;
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                                                                                                                                                                                                                                                                             NAME/KEY: misc_binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
                                                                                      LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_binding
CCATTON: 77046..77070
; OTHER INFORMATION: 20-853-415.probe
US-09-756-580-1
                                                                                                                                                                                                                                                               OTHER INFORMATION: 20-841-149.probe
                                                                                                                                                      OTHER INFORMATION: 17-42-319, probe NAME/KEY: misc_binding LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250, probe
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Patent No. 5703220
INFORMATION: 20-853-415.mis
(EY: primer_bind
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compailble
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TELECOMMUNICATION INFORMATION:
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APPLICANT: Gantz, Ira
TITLE OF INVENTION: Genes En
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NAME: Smith, Deann F.
REGISTRATION NUMBER: 366E
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Best Local Similarity 61.7
Matches 50; Conservative
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                                                                                                                   NAME/KEY: misc_binding
LOCATION: 12335..12359
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ADDRESSES: Hai
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COUNTRY:
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TYPE: nu
                    NAME/KEY:
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Gaps
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      Length 975;
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: Genes Encoding Melanocortin Receptors
                                                Indels
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Score 31.2; D3 1;
Pred. No. 5.2;
); Mismatches 108;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Tue Feb

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FILING DATE:
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                   LOCATION:
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US-08-842-238-9
   NAME/KEY:
                               US-08-842-045-9
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                                                                  Query Match
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                                                                                                                                                          0
                                                                                                                            Length 975;
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APPLICANT: Yamada, Tadataka
APPLICANT: Genera, Ira
APPLICANT: Genera, Ira
TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
NUMBER OF SEQUENCES: _23
                                                                                                                          8.9%; Score 31.2; DB 1; Length 9:
llarity 47.1%; Pred. No. 5.2;
Conservative 0; Mismatches 108; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPPRATEM: PC-DOS/KS-DOS
SOFTWARE: PatentIn Release #1.6, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harness, Dickey & Pierce, P.L.C.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (810)641-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 36683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NC
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STREET: P.O. BOX 828
CITY: Bloomfield Hills
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 975 base pairs
IYPE: nucleic acid
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                                                                            1..975
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                                                                                                                                      Local Similarity
es 96; Conserv
           ORIGINAL SOURCE:
ORGANISM: Mouse
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                                                               NAME/KEY:
ANTI-SENSE:
                                                                            ; LOCATION:
US-08-672-109B-9
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STATE: M
COUNTRY:
                                                                                                                            Query Match
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                                              Gaps
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Length 975;
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: Genes Encoding Melanocortin Receptors
8.9%; Score 31.2; DB 1; Length 9 47.1%; Pred. No. 5.2; tive 0; Mismatches 108; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,238
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NAME: Smith, Deann F. 8663
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 2115-000853DVD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               431 ATGSTGATGTACCTGTCCACCGCA 408
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; Sequence 9, Application US/08842238
; Patent No. 5869257
; GENDRAL INFORMATION:
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: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (810)641-0270
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: P.O. Box 828
CITY: Bloomfield Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           975 base pairs nucleic acid
                 Best Local Similarity 47.13
Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yamada, Jadat APPLICANT: Gantz, Ira APPLICANT: Gantz, Ira TILLE OF INVENTION: General NUMBER OF SEGUENCES: 23 CORRESPONDENCE ADDRESS:
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MOLECULE TYPE:
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IIILE OF INVENTION: Methods and Reagents for Discovering and IIILE OF INVENTION: Using Mammalian Melanocortin Receptor Agorists and Antagoni IIILE OF INVENTION: To Modulate Feeding Behavior in Animals
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   TTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAATCTATAAAAGGAACTAGTCCCG 250
                                                                                                           551 TIGGACTCATAGTAGATGATGAAACAATGCCGCAGCTTATGCAGAAGGTCCAGATGCAG 492
                                                                                                                                               251 GCAAAAACCCCGTAATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGAGTGG 310
                                                                                                                                                                     GCGATGATCACCCCCGAGCGCCTCGCGGTCATGATGTGGTAGCGCAAGGCATAGAAG 432
                                     611 AGAGACACCATGAAGAACAGCATGGTGAAGAAGATGGAGATGAGGCAAATGATCACATAC 552
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STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENI APPLICATION DATA: US/08/706.281A
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Pred. No. 5.2;
0; Mismatches 108;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-706-281A-17/c
Sequence 17, Application US/08706281A
Patent No. 6100048
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cone, Roger D
APPLICANT: Fan, Wei
APPLICANT: Boston, Bruce A
APPLICANT: Kesterton, Robert A
APPLICANT: Lu, Dongsi
APPLICANT: Chen, Wenbiao
                                                                                                                                                                                                                                         431 ATGTGATGTACCTGTCCACCGCA 408
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Best Local Similarity 47.1%;
Matches 96; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 312-913-00C1
312-913-0002
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LENGTH: 978 base pairs
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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TELEFAX: 3
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US-08-706-281A-17
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COUNTRY:
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                                                                   GCAAAAACCCCGTAATTGCGAGCGAGGGAGTGAGTGGGGGCCGGGACCCGCAGAGCCGAGCCG 310
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                                                                                                                                         TITGACCGATAGTAACCICTGCGCTCGGTGCAGCCGAATCTATAAAAGGAACTAGICCCG 250
                                                                                                       611 AGAGACACCATGAAGAACAGCATGGTGAAGAACATGGAGATGAGGCAAATGATCACATAC 552
                                     Gaps
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Length 975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genes Encoding Melanocortin Receptors
8.9%; Score 31.2; DB 2; Length 9
47.1%; Pred. No. 5.2;
Live 0; Mismatches 108; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dickey & Pierce, P.L.C.
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FILING DATE: July 23, 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08629335B Patent No. 6117975
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      431 ATCCTGATGTACCTGTCCACCGCA 408
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NAME: Smith, Deann F.
REGISTRATION NUMBER: 36633
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
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TELEFAX: (810)641-0270
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 975 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bloomfield Hills
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Best Local Similarity 47.1
Matches 96, Conservative
                                   Conservative
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TITLE OF INVENTION: Ge:
NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
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APPLICANT: Gantz, I
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                Similarity
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ORGANISM: Mouse
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Query Match
Best Local Simi
Matches 96;
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                                                               GCGATGATCACCCCCGAGCGCCTCGCGGTCATGATGTTGGTAGCGCAAGGCAAAGAAGAA
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                                            TITIGACCGATAGTAACCTCTGCGCTCGGTGCAGCGAATCTATAAAAGGAACTAGTCCCG
                                                                                                        Low, Malcolm J
TITLE OF INVENTION: Mammalian Melanocortin Receptor and Uses
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.9%; Score 31.2; DB 4; Length 978;
llarity 47.1%; Pred. No. 5.2;
Conservative 0; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDING TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: 9C-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 12-Jun-1998
CLASSIFICATION: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
RAME: NO. 6278038nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . SEQUENCE DESCRIPTION: SEQ ID NO: 17: US-09-097-231-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                   RESULT 15
US-09-097-231-17/c
; Sequence 17, Application US/09097231
; Patent No. 6278038
; Patent No. 6278038
                                                                                                                                                                                       ACCCTTCTCTCCGGGCTGCGGCA 334
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TELEFAX: 312-913-0002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 978 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "ELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                          APPLICANT: Cone, Roger D
Chen, Wenbiao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90909
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Best Local Similarity
Matches 96; Conserv
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Db 551 TTGGACTCATAGTAGATGATGAGAGATGCCGCAGCTTATGCAGAGGTCCAAATGCAG 492

Qy 251 GCAAAAACCCGTAATTGCGAGCGAGAGTGGGGCCGGGACCGCAGCCG 310

Qy 311 ACCTTCTCCCGGGCTCGCGGTCATGTGTGTGGTGGTAGCGCAAGGCATAGAG 432

Qy 311 ACCTTCTCCCGGGCTGCGGCA 334

Db 431 ATGGTGATGTACCTATCCACGCA 408

Search completed: Pebruary 3, 2003, 21:02:27

Job time: 98.5211 secs
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7959.555 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                08-09-596-1410-3_COPY_1292_1643
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                             Title:
Perfect score:
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2_5/ptodata/1/pubpna/US60_NEW_PUB.seg:*/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seg:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SHIMMARIES

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Result No	2000		s Ouery Match Length	Ľ	Ę.	
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. 1	c	95.3	3231	10	US-09-846-456-1	Sequence 1, Appli
. 4	244	69.4	2893	10	US-09-845-456-3	Sequence 3, Appli
	3 91	CI	221	10	JS-09-845-456-4	4
7	1 36.2	10.3	1102	10	US-09-833-381-1386	1386,
C)	5 31.4		373	10	US-09-880-107-1039	
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O	7 31.4		2060	10	US-09-954-456-1804	
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U	9 31.4		81001		US-09-751-877-1	Secuence 1, Appli
Ä	31.	8.9	52216		US-09-747-81C-1	
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	30.8		10144		US-09-880-107-2169	2168
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ī	0	60	270		US-09-783-590-169	169
et	\circ		42999	9	US-09-759-462A-17	Sequence 17, Appl
ũ	0		42999		US-10-125-767-17	Sequence 17, Appl
Či O	9 29.8		15515		US-09-822-860-3	'n

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Sequence 1450, App Sequence 147, Appli Sequence 360, App	the ABC1 Gene, Molecules Modifying ses	10; Length 3231; 9; 1; Indels 5; Gaps 1;
US-09-867-701-87 US-09-764-870-14 US-09-764-870-14 US-10-918-350 US-09-989-735-560 US-09-989-735-360 US-09-989-735-360 US-09-989-735-360 US-09-991-181-360 US-09-993-687-350 US-09-993-687-350 US-09-993-687-350 US-09-989-722-369 US-10-174-599-239 US-09-989-722-360 US-09-9991-0732-360 US-09-9991-0732-360 US-09-9991-0732-360 US-09-9991-0732-360 US-09-9991-0732-360 US-09-9991-0732-360 US-09-9991-0732-360 US-09-9991-0732-360 US-09-9991-0732-360	rs id for	Score 335.4; DB Pred. No. 1.5e-8 0; Mismatches
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	ESULT 1 Sequence 1, Application US/09845456 Patent No. US20020146792A1 GERERAL INFORMATION: APPLICANT: Prades, Catherine APPLICANT: Prades, Catherine APPLICANT: Denefile, Patrice APPLICANT: Denefile, Patrice APPLICANT: Denefile, Patrice APPLICANT: Brewer, Bryan APPLICANT: Brewer, Bryan APPLICANT: Remaley, Alan APPLICANT: Brewer, Bryan APPLICANT: Remaley, Alan APPLICANT	95.3%; imilarity 98.3%; Conservative
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-09-846-456-1 Sequence 1, Applicat GENERAL INFORMATION APPLICANT: Rosier, APPLICANT: Rosier, APPLICANT: Prades, APPLICANT: Ponetle APPLICANT: Denefle APPLICANT: Brewer, APPLICANTON: CURRENT APPLICATION CURRENT APPLICATION CURRENT APPLICATION SEQ. ID NO SOFTWARE: PATENTING DATE: PRIOR PILING DATE: CURRENT: SA31 LENTH: 3231 TYPE: DNA CUSCANTSM: Homo Sapus-	Query Match Best Local Similarity Matches 351; Conser

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TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying TITLE OF INVENTION: Activity and Therapeutic Uses
FILE REPERBACE: 3866.0565
CURRENT APPLICATION NUMBER: US/09/846,456
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 50/201,280
PRIOR PILING DATE: 2000-05-02
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SETTLE OF INVENTION: Keith E.
TITLE OF INVENTION: NO. US2020132090Alel Nucleic Acid and Protein Homologs FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
FRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: ESSUED IO Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 TGGGCGGCTGAACGTCGCCCGTTTAAGGGGCGGGCCCCGGGCTCCACGTGCTTTCTGCTGA 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 25.9%; Score 31; DB 10; Length 221; Best Local Similarity 100.0%; Pred. No. 5.8e-18; Matches 91; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 CCGGGCTGCGGCAGGCAGGCGGGGGAGCTC 352
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; OTHER INFORMATION: n = A, E, C or G
US-09-833-381-1386
                                                                                                                                                                                                                                                                                                                                         version 3.0
                                                      Praces, Catherine
                                                                   Lemoine, Cendrine
Naudin, Laurent
                                                                                                                       Duverger, Nicolas
                                                                                                        Denefle, Patrice
                                                                                                                                          Brewer, Bryan
Remaley, Alan
Fojo, Silvia
US20020146792A1
                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-0
NUMBER OF SEQ ID NOS: 20
                                   APPLICANT: Rosier, Marie
                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-846-456-4
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Matches 109; Conserv
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                  GENERAL INFORMATION:
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NGTH: 1102
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APPLICANT:
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APPLICANT:
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                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fojo, Silvia
TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying
TITLE OF INVENTION: Activity and Therapeutic Uses
FILE REFERENCE: 3806.0505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ;
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                                                                                                                       176 AGGGAGAGCACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAATCTATAA 235
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Pred. No. 9.7e-63;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/201,280 FRIOR FILING DATE: 2000-05-02 NUMBER OF SEQ ID NOS: 20
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Patent No. US20020146792A1
                                                                                                                                                                                                                                                                                                                                                                                     Prades, Catherine
Lemoine, Candrine
Naudin, Laurent
Deneffe, Patrice
Breer, Nicolas
Brewer, Bryan
Remaley, Alan
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Best Local Similarity 97.7%;
Matches 260; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Rosier, Marie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Home sapiens
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US-09-846-456-4
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US-09-846-456-3
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APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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SOFTWARE: FastSEQ for Windows Version 4.3 SEQ ID NO 817 LENGTH: 1704
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                                                                                                                                     ; LOCATION: (1)...(1704)
; OTHER INFORMATION: n = A,T,C or G
US-C9-834-975-817
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                                                                                                                NAME/KEY: misc_feature
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                                                                                                                                   (1704)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-09-954-456-1804/c
                                                       TYPE: DNA
ORGANISM: HOMO
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                                                                                                                                   LOCATION:
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                                                                                              FEATURE:
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APPLICANT: Van Ruffel, Christophe
TITLE OF INVENTION: NOYEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REFERENCE: MRI-016B
CORRENT APPLICATION NUMBER: US/09/834,975
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                                                       97 AGGGGGGGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAACAGAGGC 156
                                   725 TCAGGGGATCCAGGTCCCCCGGTATGGCGGACAGCCCAAGCT-CAAGAGCAGTCGGCAGA 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 CCCACCCACCTCCCCCAACTCCCTAGATGTCGTGGGCGGCTGAACGTCGCCCGTTTA 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 GGGGCAGGGCCCTCACTCTCGGCCCTGGTGTGGGGGAGAGTGAGGGGTTGGGGGAT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / OTHER INFORMATION: Genbank Accession No. US20020142981A1 AA435662
US-09-880-107-1039
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                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Expression Profiles in
FILE OF INVENTION: Gene Expression Profiles in
FILE REFERENCE: 44921-5025-W0
CURRENT APPLICATION UNBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR PAPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-10-10
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Local Similarity 49.7%; pred. No. 3;
Nes 50; Conservative 0; Mismatches
                                                                                                          192 ITGACCGATAGTAACCTCTGCGCTCGGTGCAGC 224
                                                                                                                                               844 GGGCTGGGGGGGCCAGCCGGCGCTCGGGGAGGC 376
                                                                                                                                                                                                                                         Sequence 1039, Application US/09880107
Patent No. US20020142981A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DAIE: 2001-04-13
PRICK APPLICATION NUMBER: 60/197,538
PRICK FILING DATE: 200C-04-14
NUMBER OF SEQ ID NOS: 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 817, Application US/09834975 Patent No. US20020110815A1
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SEQ ID NO 1039
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APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IYPE: DNA
ORGANISM: Homo sapiens
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US-09-880-107-1039/c
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Matches
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GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
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                                                                                                                              269 CGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCCCCGGGCT 328
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      Length 1704;
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      DB 10;
Query Match
8.9%; Score 31.4; Di
Best Local Similarity 61.7%; Pred. No. 5;
Matches 50; Conservative 0; Mismatches
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53.7%; Pred. No. 5.3;
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CURRENT FILING DATE: 200-09-18
PRIOR FILING DATE: 200-09-18
PRIOR FILING DATE: 200-09-18
PRIOR FILING DATE: 200-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-26
PRIOR PRILING DATE: 2000-09-26
PRIOR PRILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR PRILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
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OTHER INFORMATION: 20-828-311.mis
NAME/KSY: primer_bind
LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
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                                                                                                                                                                                                           LOCATION: 15969..17969
OTHER INFORMATION: 3'regulatory region
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NAME/KEY: primer_bind
LOCATION: 929..949
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NAME/KEX: primer bind
LOCATION: 42572...42591
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OTHER INFORMATION: 20-841-149
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NAME/KEY: primer bind
LOCATION: 15469..1540
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OTHER INFORMATION: 20-828-311
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NAME/KEY: primer_bind
LOCATION: 45328..45347
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NAME/KEY: primer_bind
LOCATION: 76644..76654
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OTHER INFORMATION: 20-853.rp
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NAME/KEY: aliele
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NAME/KEY: primer_bind
LOCATION: 45863..45883
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INFORMATION: 17-42.pu
                                                          OTHER INFORMATION: excn 2
                                                                                              ON: 13641..13752
INFORMATION: exon 3
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OTHER INFORMATION: exon
                  NAME/KSY: exon
LOCATION: 13470..13526
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LOCATION: 77166..77189
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LOCATION: 12029...205
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LOCATION: 77058
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                                                                            NAME/KEY: exon
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APPLICANT: Ebbets-Reed, Dana
APPLICANT: Ebbets-Reed, Dana
APPLICANT: Salter-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWIH
FILE REFERENCE: 89.033.REG
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEO ID NOS: 1510
SOFIWARE: Patentin Ver. 2.0
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Duciert, Aymeric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (491)
OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: 5'regulatory region
                                                                                                                                                                     Sequence 142, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
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Bour, Barbara
Bihain, Bernard
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LOCATION: 12947..12958
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FEATURE:
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US-09-751-877-1/C
                                                                                                                                RESULT 8
US-09-764-868-142
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LENGTH: 2928
                                                                        1299 C 1299
                                    121 C 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 GCTCGGTGCAGCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCGTAATTGCGAG 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Steve Ruben TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.8%; Score 31; DB 1
Best Local Similarity 60.5%; Pred. No. 6.6;
Matches 49; Conservative 1; Mismatches
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                                                                                                                                                                                                                                                                  Score 31.2; I
Pred. No. 18;
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CURRENT PAPLICATION NUMBER: US/09/925,3C0

CURRENT FILING DATE: 2001-08-.0

PRIOR APPLICATION NUMBER: PCI/US00/05988

PRIOR FILING DATE: 200-03-08

PRIOR FILING DATE: 200-03-08

PRIOR FILING DATE: 1999-03-12
    CURRENT APPLICATION NUMBER: US/09/747,810 CURRENT FILING DATE: 2000-12-22
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US-09-925-300-320
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OTHER INROGARTION: n equals a,t,g, or
NAME/KBY: misc feature
LOCATION: (1733)
OTHER INFORMATION: n equals a,t,g, or
NAME/KBY: misc feature
LOCATION: (1750)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 320, Application US/09925300 Patent No. US20020151681A1
                                          PRIOR APPLICATION NUMBER: 60/173,003
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30393 TGAGAGTGGGATGGGCCAGG 30412
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                                                                                                                                                                                                                                                                  8.9%;
51.4%;
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OTHER INFORMATION: n equals
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 320
                                                                                                                                                                                                                                                                Query Match 8.99
Best Local Similarity 51.49
Matches 72; Conservative
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                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Craig Rosen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                    TYPE: DNA
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                                                                                                                  SEQ ID NO LENGIE:
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TITLE OF INVENTION: A METHOD FOR ISOLATING AND PURIFYING MULTIPOTENTIAL NEURAL PROGEN
TITLE OF INVENTION: CELLS AND MULTIPOTENTIAL NEURAL PROGENITOR CELLS
FILE REFERRORE: 19603/3580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                  LOCATION: 15242.715260

COTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer_bind
LOCATION: 42199.42217

OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer_bind
LOCATION: 42219.42237

OTHER INFORMATION: 20-841-149.mis
COCATION: 42219.42237

OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer_bind
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NAME/CRY: primmer_blod
OTHER INFORMATION: 20-842-115.mis complement
NAME/CRY: primmer_blod
NAME/CRY: primmer_blod
OTHER INFORMATION: 20-853-415.mis
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LOCATION: 77359..77077
OTHER INFORMATION: 20-853-415.mis complement
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Pred. No. 18;
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                                                                                                               OTHER INFORMATION: 17-42-319.mis complement NAME/KEY: primer_bind
LOCATION: 15222..15240
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LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: 20-853-415.probe US-09-751-877-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: 20-828-311.probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 42206.,42230
OTHER INFORMATION: 20-841-149.probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: 17-42-319.probe NAME/KEY: misc_binding LOCATION: 15229.15253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: 17-41-250.probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09747810
Patent No. US20020612903A1
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                                                                                                                                                                                OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
LOCATION: 15242..15260
NAME/KEY: primer_bind
LOCATION: 12238.12346
OTHER INPORMATION: 17-42-319.mis
NAME/KEY: primer_bind
LOCATION: 12348.12366
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Best Local Similarity 61.7%;
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APPLICANT: Goldman, Steven A.
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LOCATION: 1227..1251
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LOCATION: 77046..77070
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US-09-747-810-1
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150 CAGAGGCCGGGAACGGGGCGGGGAGGAGGAAGCACACAGGCTTTGACCGATAGTAACCTC 209
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SEQ ID NO 2577
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Best Local Similarity
Matches 81; Conserv
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult FALM or file wrapper NUMBER OF SEQ ID NOS: 2003
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1616
                                                                                                                                                                                                                                                               in Liver Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
, APPLICANT: Rosen et al.
, TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
, FILE REFERENCE: PC009
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                                                                                                                                                                                           APPLICANT: WOCKIE, JOSEPH G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in
TITLE OF INVENTION: Gene Expression Profiles in
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT APPLICATION NUMBER: US 60/211,379
PRIOR PLING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-10
RROR FILING DATE: 2000-10-02
KUNBER OF SEQ ID NGS: 3950
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 48.3%; Pred. No. 14;
Matches 86; Conservative 0; Mismatches
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47.8%; Pred. No. 14;
live 0; Mismatches
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; LOCAITON: (1)..(10144)
US-09-880-107-2168
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Patent No. US20020132767A1
                                                                                                                   Sequence 2158, Application US/09880107
Patent No. US20020142981A1
125 CGCCGGGCCGGCGGCGA 105
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Matches 89; Conservative
                                                                                                                                                                              APPLICANT: Horne, Darci T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                           ; GENERAL INFORMATION:
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US-09-764-847-1516
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GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with TITLE OF INVENTION: Dants
FILE REFERENCE: 38-21(15401)8
CURRENT APPLICATION UNMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR FILING DATE: 1999-06-14
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APPLICANT: GAN, Weiniu
IITLE OF INVENTION:
ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
IITLE OF INVENTION: THEREOF
IITLE OF INVENTION: THEREOF
IITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/09/816,095
CURRENT APPLICATION NUMBER: US/09/816,095
CURRENT FILING DATE: 2001-03-26
NUMBER: FASTERO FOR WINDOWS Version 4.0
SEQ ID NO 3
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Pred. No. 5;
0: Mismatches 84;
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): OTHER INFORMATION: Clone ID: LIB3028-023-Q1-B1-C3
US-09-878-574-2577
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Patent No. US20020137164A1
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| TYPE: DAA | TYPE
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Search completed: February 3, 2003, 16:33:24 Job time : 152.868 secs

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BE272078 601140866
BE258315 601114804
BE387797 601282966
BI193161 602947133
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( Dases 1 to 1863)
Smith,J., Bruley,C.K., Paton,I.R., Dunn,I., Jones,C.T., Windsor,D., Morrice,D.R., Law,A.S., Masabanda,J., Sazanov,A., Waddington,D., Pites,R. and Burt,D.W.

Differences in gene density on chicken macrochromosomes and
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BM451890 AGENCOURT
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BG770188 602744953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 1863)
Smith,J., Bruley,C.K., Paton,I.R., Law,A.S., Masabanda,J.,
Waddingtos,D., Fries,R. and Burt,D.W.
Direct Submission
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1863 bp DNA linear GSS
Gallus gallus anonymous sequence from Cosmid mapping to
microchromosome (Cosmid 20 - Contig 12), genomic survey
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Copyright (c) 1993 - 2003 Compuc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: nelsayed@tigr.org
Details of T. brucel sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
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                                                                                                                                                                                         Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Earris, B., El-Sayed, N., Hou, L., Melville, S.S., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
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Eukaryota; Euglenozoa; Xinetoplastica; Trypanosomatidae;
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                                                                                                                    Length 1863;
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Pred. No. 4.5;
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/strain="TREU927"
                                              /chromosome="microchromosome" 392 c 580 g 482 t
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            /organism="Gallus gallus"
/db_xref="taxon:9031"
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JG256511 962 3D MRNA linear ESI 13-FEB-2001 602370051F1 NIH_MGC_92 Homo sapiens CDNA clone IMAGE:4478196 5', MRNA sequence.
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ZF637-2-002123 Zebrafish shield stage whole embryo cDNA library
MPMGp637 Danio rerio cDNA clone MPMGp637_7P1;MPMGp6372017 5', MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
    Tissie procurement: Arcc
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clope distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/Link at:
    http://image.llnl.gov
    Plate: LibM10308 row: e column: 13
    Figh quality sequence start: 2
    Figh quality sequence start: 2
    Figh quality sequence start: 3
    Figh quality sequence start: 3
    Figh quality sequence start: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="embryonal carcinoma, cell line"
//lab_host="DH10B (phage-resistant)"
//note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dr primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Wetazoa, Chordata, Craniata, Vertebrata, Buteleosto Mammaila, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 962)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 GIGCTTTCTGCTGAGTGACTGAACTACATAAACAGAGGCCGGGAACGGGGCGGGGAGGAG
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88 CITTGACCGATAGIAACCICTGCGCTCGGTGCAGCCGAATCT 129
                         197 GTTTGACCGCTCCTAACCACTAGTTTTGATTGTACCAACTCT 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32.8; DB
Pred. No. 18;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4478196"
/clone_lib="NIH_MGC_92"
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                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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Best Local Similarity
Matches 46; Conserv:
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human.
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Best Local S
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AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /issue_type="whole embryo"
/dev_stage="shield stage, 6 hrs post_fertilisation"
/dev_stage="shield stage, 6 hrs post_fertilisation"
/lab_stage="coli, XLi blue MRF"
/note="vector: psportl; Site_1: Not!; Site_2: Sall;
/note="vector: psportl; Site_1: Not!; Site_2: Sall;
/lote="vector: psportl; Site_1: Not! Site_2: Sall;
/lote="vector: psportl; Site_1: Not!"
/lote="vector: psp
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0
                     Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                  Contact: Seon's (2001)
Contact: Seon's (2001)
Contact: Seon's (2001)
Max-Planck Institut Fuer Molekulare Genetik
Innextr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 162
Fax: +49 30 8413 180
Email: hennig@molgen.mpg.de
5' EST sequencing of clones from a zebrafish shield stage library,
normalised from 55,000 starting clones by oligonucleotide
                                                                                                                                                            Clark, Aanstad, Hennig, S., Johnson, S.L. and Lehrach, H. EST sequencing of a zebrafish shield stage cDNA library normalised by oligorucleotide fingerprinting
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1 (bases 1 to 513)
Kahairas, G.C., Wallace, J.C., Smith, K., Swartzeil, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 GAGGCCGGGAACGGGGCGGGGAGGAAGGAAGCACAGGCTTTGACCGATAGTAACCTCTG 109
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/clone="mpWcp637_791;MPMCp637P017"
/clone=lib="zebrafish shield stage whole embryo cDNA
library MPMGp637"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13; Length 712;
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401 Queen Anne Avenue North, Seattle, WA 98109, USA
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High Throughput Sequencing Center
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High quality sequence stop: 712.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                Unpublished (2001)
                                                                                                                                      (bases 1 to 7
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                                                                                                                                      REFERENCE
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/tissue_type="maintain" from tonsils (cell line)"
/lab host="DH10B (phage-resistant)"
/note="vorgan: 3-cells; Vector: poTB7; Site_1: Xhoi;
Site_2: EcoR1: CDNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCACGAG(6): Size-selected 550bp for average insert size 18kb. Library constructed by Ling Hong in the laboratory of GeralG M. Rubin (University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                                                                  /clone="Plate=3236 Col=20 Row=E"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Cc11 DH10B"
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.
Plate: LLCM1704 row: i column: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 973)

NHF-MGC Attp://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MCC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 GAACTACATAACAGAGGCCGGGAACGGGGGGGGGGGAGGAGGAGGACACAGGCTTTGACC 95
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausherg, Ph.D.
Email: capabs-rifmail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                               11 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                                                                                                                                                                                            175 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32.2; I
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4855376"
                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NIH_MGC_48"
Tel: (205) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
                                                                                                                                                               High quality sequence stop: 513.
Location/Qualifiers
1. .513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 498
Location/Qualifiers
1. 973
                                                                                                                row: E column: 20
                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
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61.2%;
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                                                                                                             Plate: 3236 row
Class: BAC ends
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GSS 08-JUL-1999

BASE COUNT

Qγ g Š CC

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/clone_inb="RPC193-Den11"
/clone_inb="RPC193-Den11"
/clone_inb="RPC193-Den11"
/clone_inb="RPC193-Den11"
/constructed for The Institute for Genomic Research by
Constructed for The Institute for Genomic Research by
Bohui Zhao in Pieter de Jong's laboratory (Roswall Park
Cancer Institute, Buffalo, NY). Briefly, Trypanosoma
brucel TRE027/4 GUTar 10.1 agarose embedded DNA was
brucel TRE027/4 GUTar 10.1 agarose embedded DNA was
brucel TRE027/4 GUTar 10.1 agarose embedded DNA was
partially digested with a combination of Eco RI and Eco RI
methylase (RPC193-EcoRI segment) or Dpn II (RPC193-DpnII
segment). High molecular weight fragments were ligated in
pBAC03.6 vector digested with Eco RI or Bam HI,
respectively. The average insert size is 141 Kb. Total
coverage (both segments): > 90 X the haploid
non-miniciromosomal genome."
                                                                                                                                                                                                                                                                                   Trypanosoma.

I (bases I to 616)

El-Sayed,N., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
Fraser,C. and Adams,M.

Fraser,C. and Adams,M.
Use of BAC end sequences from Trypanosoma brucei GUTat 10.1 RPCI-93 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI193040 742 bp mRNA linear SST 10-JUL-2001 602947291F1 NIS_MGC_42 Homo sapiens cDNA clone IMAGE:5090326 5',
                                          FPCI93-DpnII-28C6.IV RPCI93-DplI Trypanosoma brucel genomic clone
AQ643297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: nelsayed@tigr.org
Clones and high density filters may be purchased from BACPAC
Resources (http://bhcpac.med.buffalo.edu. BAC end sequences search
page: http://www.tigr.org/tdb/mdb/tbdb/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31.6; DB 17; Length 616; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 CTTTGACCGAIAGTAACCTCTGCGCTCGGTGCAGCCGAATCT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 GTTTGACCGCTCCTAACCACTAGTTTTGATTGTACCAACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="TRSU927/4 GUTat 10.1"
/db_xref="taxon:5691"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Other_GSSs: RPC193-DpnII-28C6.TJ
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56.98;
                                                                                                                                                                     GI:5120007
                                                                                                                                                                                                                    Trypanosoma brucei.
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Class: BAC end:
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                                                                                                                                                                  AQ643297.1
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                                             AC643297/c
LOCUS
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                                                                                                                                                                     VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TA167G02P 440 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 167g02, forward sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma bruce; (TRE0927/4 GUTAt 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, fi. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@it.gr.org
Details of I brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Campus, Hinxton,
California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NH_MGC Library."
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                                                                                                                                                                                                                                                                                        793 CAGCGACGGATGCCCAGGATCAGGAGCGGAGGAGGAGGACGACGCGGGTAGCCACGACAGC 734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing
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                                                                                                                                              Length 973;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission Submitted (10-DEC-2000) Trypanosoma brucei genome seq project, Sanger Centre, The Wellcome Trust Genome Cam Cambridge CBIO 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Pred. No. 34;
0; Mismatches
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                                                                                                                                         12.9%; Score 31.8; Districty 61.4%; Pred. No. 35; Conservative 0; Mismatches
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96 c 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic survey sequence.
AL474862
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ilarity 56.9%;
Conservative
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(bases 1 to 440)
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Matches 58; Conserv
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Matches 51; (
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LOCUS DEFINITION

ACCESSION KEYWORDS SOURCE

VERSION

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

RESULT 7 TA167G02P

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Gaps

0

BASE COUNT

ORIGIN

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FEATURES

New York

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Genoscope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="InAGGE:5090326"
/clone="InAGGE:5090326"
/clone="InAGGE-472"
/tissue_type="epithelioid carcinoma cell line"
/tab_host="Dath08 (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: Xho1;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscribt II RI (Life Technologies).
Note: tals is a NIH_MGC Library. |" (Life Technologies).
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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NIH-MGC http://mgc.ncl.nim.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
                                                                                                                                              1 (bases 1 to 742)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Nopublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAACAGAGGCCGGGAA 50
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Pred. No. 38;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .742
                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                    G1:14648060
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Liarity 62.8%;
Conservative (
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BI115921
                                                                                     Homo sapiens
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Best Local Similarity
Matches 49; Conserv
BI193040
BI193040.1
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VERSION
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/GDATEST TOWN SEPTENS
/GDATEST TOWN SEPTENS
/Clone="NAGE:5015158"
/Clone="NAGE:5015158"
/Clone="Line="NGC27"
/tissue_type="smalcolor: Tell carcinoma"
/tissue_type="smalcolor: Tell carcinoma"
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/lab_host="bild08 (phage=resistant)"
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TR2 bp DNA linear GSS 12-MAY-2000

Tetraodon nigroviridis genome survey sequence I7 end of clone
218D02 of library G from Tetraodon nigroviridis, genomic survey
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Tetracdon nigroviridis
Tetracdon nigroviridis
Tetracdon nigroviridis
Tetracdon nigroviridis
Eukaryota: Metazca: Chordata; Craniata; Vertebrata; Bureleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Charaterization and repeat analysis of the compact genome of the
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The L.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov
Plate: LLCMi&23 row: j column: 23
High quality sequence stop: 500.
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1 (bases 1 to 782)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L.,
Bernot, A., Fizames. C., Wincker, P., Brottier, P., Quetier
Saurin, W. and Weissenbach, J.
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62.8%; Pred. No. 39;
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1. 808
/organism="Homo sapiens"
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DNA
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(8)
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                            This sequence is a single read and was generated as part of a large scale close-end sequencing project of the Tetraodon nigrovizidis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library and library availability, please contact Pieter de Jong
(bdejong&mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seg primer: 17
Seg primer: 17
Class: BAC ends.
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Bukaryota; Metazoa; Chordara; Craniata; Vertebrata; Euteleostomi;

Maala; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae
                                                                                                                                                                                                                                                                                                                                                               /close_lib="G"
/note="Genoscope sequence ID : COAG218DB01LP1-end : T7"
250 c 202 g 179 t 6 others
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            425 GOGCNGCGGCTGCCGCTGCTGCTGCTCTGGACTATATCAACACACGCGGTGGG 366
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                                                                                                                                                                                                                                                                  /crganism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="218D02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.6%; Score 31.4; DB 17; 56.6%; Pred. No. 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CGGGGCGGGGGGGGGGGGGCGTTTGACCGATA 99
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/clone="RPCI-24-305E21"
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/sex="Male"
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1. .437
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Direct Submission
Submitted (12-APR-2000)
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Jab_Lost="DH-108"

Jab_Lost="DH-108"

Jab_Lost="Wector: pCMVsport7.neo: Site_1: NotI; Site_2: Sall

Jab_Lost="Wector: pCMVsport7.neo: Site_1: NotI; Site_2: Sall

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Washington
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O
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BAHT, sites using Mbo! partially digested male C57BL/6J
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/clone_lib="Trichinella spiralis ML CMVsport jasmer"
/dev_stage="muscle stage larvae"
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Contact: McCarter JP
Washington Univ. Nematode EST Project, 1999
Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108, USA
Tel: 312 286 1800
Fax: 314 286 1800
Fax: 34 286 
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Trichinellidae; Trichinella.
1 (bases 1 to 529)
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Pred. No. 44;
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High quality sequence stop: 422.
Location/Qualifiers
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.eagues at Washington State University. DNA Sequencing Washington University Genome Sequencing Center St.
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Site_2: ECORI; CDNA made by oligo-dT priming.

Site_2: ECORI; CDNA made by oligo-dT priming.

Site_2: Acord of the second of t
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 875)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                          BI193879 875 bp mRNA linear EST 10-JU
602948207F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5991625
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. m column: 02
High quality sequence stop: 738.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                               71 AGGAGGGAGGACACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAA 125
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/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
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/db_xref="taxon:9606"
/clone="IMAGE:5091625"
/clone_lib="NIH_MGC_42"
                                                                                                                                                                               Query Match
22.4%; Score 31.2;
Best Local Similarity 54.3%; Pred. No. 46
Matches 63; Conservative 0; Mismatche
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Adams, Lucitor, Entracts, Continues, Continu
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Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
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                                       GCGGGGAGGAGGAGCACACGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCG 124
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9712 Medical Center Drive, Rockville, MD 2085C USA
Tel: 3018699056
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/db_xref="ATCC (inhost):125343"
/db_xref="taxon:9606"
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/tissue_type="cerebellum"
/dev_stage="adult"
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Pred. No. 55
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Search completed: February 4, 2003, 03:27:17 Job time : 277.726 secs

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. /cgn2_b/ptodata_//ina_/FD_COMB.seq:*
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          GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-762-227A-70
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PCT-US95-01185-70
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APPLICAWT: Davis, Roger J.
APPLICANT: Galcheva-Gargova, Zoya
TITLE OF INVENTION: NON-ACTIVATED RECEPTOR COMPLEX
NUMBER OF SEQUENCES: 35
CORRESPONDENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30; DB 2;
Pred. No. 0.52;
0; Mismatches 30
US-09-103-840A-1

US-09-188-930-72

US-08-821-12

US-08-62-972A-6

US-08-62-972A-6

US-08-62-972A-6

US-08-57-972A-6

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06-JUN-1997
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FILING DATE: 06-JUN-1997
PAIOR APPLICATION DATA:
PAPELICATION NUMBER: 60/019,21
FILING DATE: 06-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: FASSE, Feber J.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 0402
TELECOMMUNICATION INFORMATION:
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TELERAX: 617/542-8906
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                                                                                          COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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OTHER INFORMATION: 20-841-149 : polymorphic base A or G
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                                                                         : polymorphic base A or
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CTERN INFORMATION: 20-641-149.mis

NAME/KEY: primer_bind

LOCATION: 42219.42237

CTERN INFORMATION: 20-841-149.mis complement

NAME/KEY: primer_bind

LOCATION: 45422.49441

CTERN INFORMATION: 20-842-115.mis

NAME/KEY: primer_bind

LOCATION: 45443.45461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: 20-828-311.mis complement NAME/KEY: princt-bind LCOATION: 12328.12346 OTHER INFORMATION: 17-42-319.mis NAME/KEY: princt-bind LCOATION: 17-42-319.mis COMPLET INFORMATION: 17-42-319.mis complement OTHER INFORMATION: 17-42-319.mis complement
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OTHER INFORMATION: 20-842-115.mis complement
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INFORMATION: 17-41-250.mis complement
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COTHER INFORMATION: 20-828-311.mis NAME/KEY: primer_bind LOCATION: 1240..1258
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NAME/XEY: primer_bind
LOCATION: 14992..15012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: primer_bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-441.rp complement
NAME/KEY: primer bind
LOCATION: 42070..42090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: 20-841.pu
NAME/KEY: primer_bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.xp oc
NAME/KEY: primer_bind
LOCATION: 45328..45347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 45863...45883
OTHER INPORMATION: 20-842.rp
NAME/KEY: primer_bind
LOCATION: 76644...7664
OTHER INPORMATION: 20-853.pu
NAME/KEY: primer_bind
LOCATION: 77166...77185
                                                                       DIHER INFORMATION: 20-842-115
                                                                                                                  LOCATION: 77058
OTHER INFORMATION: 20-853-415
                                                                                                                                                                                                                                                     LOCATION: 1357..1377
OTHER INFORMATION: 20-828.rp
                                                                                                                                                                                     LOCATION: 929.,949
OTHER INFORMATION: 20-828.pu
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OTHER INFORMATION: 20-842.pu
                                                                                                                                                                                                                                                                                                                     LOCATION: 12029. 12050
OTHER INFORMATION: 17-42.pu
NAME/KEY: primer_bind
LOCATION: 12581..12603
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LOCATION: 15222..1524(
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LOCATION: 1357..1
                                                                                            NAME/KEY: allele
LOCATION: 77058
                                                                                                                                                                                                                                                                                                  NAME/KEY:
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APPLICANT: Bougueieret, Lydie
APPLICANT: Bobes-Reed, Dana
APPLICANT: Salter-Cid, Luisa
APPLICANT: Salter-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89.US2.CIP
160 GGGCIGCTGCTCGTCCTCGGCGCTGATGGGCCGGAACAGGIGATCAGGGGCAGGCGG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : polymorphic base C or I
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                                                                                                                                                                                                                                                                                                                                                              Dumas Milne Edwards, Jean-Baptiste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: PCT/IB00/0101
PRIOR FILING DATE: 2000-06-22
PRIOR PAPLICATION NUMBER: PCT/IB99/02058
PRIOR APPLICATION NUMBER: PCT/IB99/02058
PRIOR FILING DATE: 1999-12-20
PRIOR PELING DATE: 1999-12-21
PRIOR PELING DATE: 1999-12-22
PRIOR PILING DATE: 1999-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 89.US2.CIP
CURRENT APPLICATION NUMBER: US/09/750.580
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 09/599,362
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PRIOR APPLICATION NUMBER: US 60/141,032
MARKOR FILING DATE: 1999-06-25
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LOCATION: 10946..12946
OTHER INFORMATION: 5'regulatory region
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OTHER INFORMATION: 3'regulatory region
                                                                                                                                                                                                   Sequence 1, Application 35/09750580 Patent No. 6455280 GENERAL INFORMATION:
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                                                                     100 CGGGCCGGGCGGCGA 83
                                        61 CGGGCGGGGAGGGA 78
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Denison, 3lake
Bour, Barbara
Bihain, Bernard
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NAME/KEY: misc_feature
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LOCATION: 13470..13526
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LOCATION: 13641..13752
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LOCATION: 12947..12958
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NUMBER OF SEQ ID NOS:
SOFTWARE: Patent.pm
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LOCATION: 1239
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LOCATION: 15241
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LOCATION: 42218
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SEQ ID NO 1
LENGTH: 81001
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US-09-750-580-1/c
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APPLICANT:
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STATE: D.C.
COUNTRY: USA
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                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
LIBRARY: BRAIT(
CLONE: 1396833
CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-212-247C-3/c
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                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                        US-09-276-531-56
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APPLICANT: Gedgler, Karl J.
APPLICANT: Geogler, Karl J.
APPLICANT: Geogler, Mariah R.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17479 GGCCTGCTGCTCCTCGCGCTGATGGGCCCGAACAGGTGATCAGGGCAGGCG 17420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGCCCGGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTAAAACAGAGGCCGGGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30; DB 4; Length 81001;
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          COCATION: 77059, 77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: 9715m-120707
COCATION: 77059, 77077
OTHER INFORMATION: 20-853-415.mis complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.9;
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                                                                                                      NAMEYREY: MISC_BIRGING CONTROL 227, 1251
CTGER INFORMATION: 20.829-311.probe
NAMEYREY: MISC_BIRGING CONTROL 12335, 12359
LOCATION: 12335, 12359
COTHER INFORMATION: 17-42-319.probe
NAMEYREY: MISC_BIRGING CONTROL 15229, 15239
OTHER INFORMATION: 17-41-250.probe
NAMEYREY: MISC_BIRGING CONTROL NOT CONTROL 15229, 15239
LOCATION: 42206, 42230
OTHER INFORMATION: 20-841-149.probe
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                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: 20-842-115.probe
                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: 20-853-415.probe US-09-750-580-1
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bandman, Olga
Lal, Preeti
Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
PLILING DATE: MATCH 27, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DP 17419 CGGGGCGGGGGGGG 17402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.6%;
61.5%;
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Best Local Similarity 61.5
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_binding LOCATION: 45430..45454
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LOCATION: 77046..77070
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CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94304
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APPLICANT:
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STATE: CA
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APPLICANT:
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and GARCIA, Maria Angeles Santos
TITLE OF INVENTION: Genes of purine biosynthesis from Ashbya Gossypii
and the use thereof in microbial riboflavin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1211 GGCTGGGTATTCCCTACCTTTCTGGTCTCTGAGAGTTTACCTCCTAGAAAGTCCTCC 1270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANI: POMPEJUS, Markus; SUBIBERGER, Harald; JOEFFKEN, Hans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.4%; Score 28.4; DB 4; Length 1610; 53.6%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 GGGGCGGGGAGGAGGAGGCACAGGCTTTGACCGATAGTAACCTCTGCG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette, 3.5 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storag COMPUTER: LBM AT-compactible, Pentium processor CPEATING SYSTEM: Windows 95 SOFTWARE: WordPerfect version 6.1 CURREWT APPLICATION DATA: APPLICATION NDATA: US/09/212,247C FILING DATE: 16-Dec-1998 CLASSIFICATION: <Unknown>
INFORWATION FOR SEQ. ID NO: 3: SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Kell & Weinkauf
STRETT: 1101 Connecticut Avenue
CITY: Washington
ATTORNEY/AGENT INFORMATION:
NAME: Lynn E. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0008 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09212247C Patent No. 6391603 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthesis
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20036
COMPUTER READABLE FORM:
                                                                                                                            TELEPHONE: (650) 855-05E TELEFAX: (650) 845-4166 INFORMATION FOR SEQ ID NO: 5 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           1610 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 53.67
Matches 59; Conservative
                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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75 GGAGAGCACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAATCTATAAAA 135
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REPERENCE/POCKET NUMBER: 229/182
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-160
TELEFRAX: (213) 955-0440
TELEFRAX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
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; Sequence 68, Application US/08469318
; Patent No. 6022535
                                                                                                                                                                                                                          Sequence 2, Application US/C8976255; Patent No. 6136581; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 62.7%;
Matches 42; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 5267 base pairs
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PRIOR APPLICATION DATA:
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TOPOLOGY: !!near
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
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                                                                                                                                 1346 GGA 1348
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                                                                                            136 GGA 138
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US-08-976-255-2
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APPLICANT: BERNEN, DRREN P.
APPLICANT: BAKEN, DERREN P.
APPLICANT: BAKEN, DERREN P.
APPLICANT: WILLIAMS, KEVIN P.
APPLICANT: GRGER, ELLEN A.
APPLICANT: TAYLOR, FREDENRICK R.
APPLICANT: TOWARD, JEFREREN
APPLICANT: TOWARD, JEFREREN
ITTLE OF INVENTION: METHODS
ITTLE OF INVENTION: METHODS
FILE REFREENCE: BTY 067, 01
CURRENT APPLICATION NUMBER: US/09/325,256
CURRENT PILING DATE: 1999-06-03
CURRENT PILING DATE: 1999-06-03
CURRENT APPLICATION NUMBER: 60/099,800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1226 GCSTCTCCTGCTAGAAAAGGGCAGCTTCCACCCACTGGCATGTCCGGGCAGGGAGCTG 1285
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Live 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                 33; Indels
                                                                                                                                                                                                                                                             19.6%; Score 27.2; DE 58.8%; Pred. No. 6.7; Live 0; Mismatches
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PRIOR APPLICATION NUMBER: 60/089,685
PRIOR FILING DATE: 1998-06-17
PRIOR TILING DATE: 1997-12-03
PRIOR FILING DATE: 1997-12-03
PRIOR FILING DATE: 1997-12-03
                                                                                                                                                                 NAME/KEY: 3'CTR
LOCATION: 4704..5369
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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Patent No. 6444793
                                                                                                            CDS
3588..4703
                                                                      1767..3299
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CDS
55..1482
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Best Local Similarity 58.8°
Matches 47; Conservative
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                                                         CDS
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SOFTWARE: Patentin Ver.
SEQ ID NO 11
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) LOCATION: (51)..(1283)
US-09-325-256-11
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Best Local Similarity
Matches 63; Conserva
NAME/KEY:
LOCATION:
                                                                                          FEATURE:
NAME/KEY;
                                                                                                                                 LOCATION:
                                                       NAME/KEY:
                                                                          LOCATION:
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                                     FEATURE
                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-325-256-11
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2425 CTGGGATGGGATGGGGAAGGAAGGAGGGGGGGGGGGGGTCCGGTAGTGCCCTCAGCTC 2366
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Pred. No. 7.8;
0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.D.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
CURRAIT APPLICATION DAIA:
APPLICATION NUMBER: US/28/976,255
FILING DATE: NO.6136561ember 21, 1957
                                                                                                                                                                                                                                                                                                       APPLICANT: Jono, Keith E.
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: KINASE GENES AND USES
CORRESPONDENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/031,675
FILING DATE: No. 613658lember 22, 1996
ATTORNEY/AGENT INFORMATION:
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Sarah R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,872
                                                                                                                                                                                                                                                                                                                                            Sequence 71, Application US/08469318 Patent No. 6022535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Abrams, Mark A. APPLICANT: Bauer, S. C. APPLICANT: Braford-Goldberg, APPLICANT: Caparon, Maire H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
            19.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: double
Query Match
Best Local Similarity 50.0%
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC.
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DAIE:
                                                                                                                                                                                                                                                                                                            RESULT 9
US-08-469-318-71/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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TITLE OF INVENTION: Multivariant LL-3 Hematopoiesis Fusion
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 966;
                                               Multivariant IL-3 Hematopolesis Fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                     Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
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Pred. No. 5.1;
0; Mismatches
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                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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US-08-469-318-70/c
; Sequence 70, Application US/08469318
; Patent No. 6022535
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0%;
Matches 67; Conservative
                                                                   Protein
                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                         1: 966 base pairs
nucleic acid
DEDNESS: double
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LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                    CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402 CGGGTTGATAGTAG 389
                                                                              NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 CGAATCTATAAAG 136
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                                                                                                                                                                                                        APPLICATION NUMBER:
                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                   linear
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CLASSIFICATION:
              GENERAL INFORMATION:
APPLICANT:
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                                                                                                                                    COMPUTER:
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                                                             0; Gaps
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Score 26.8; DB 3; Length 966;
Pred. No. 5.1;
0; Mismatches 67; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion TITLE OF INVENTION: Protein NUMBER OF SEQUENCES: 196
COMPUTER REALASLE FORM:
MEDIUM IYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Release #1.0, Version #1.30 (EPC)
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APPLICANT: Paik, Kumnan
Papplicant: Thomas, John W.
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (I
NUMBER OF SEQUENCES: 197
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                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.
SIREET: P. O. Box 5110
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NAMER: US/06/468,609A FILING DATE: 06-JUN-1995 CLASSIFICATION:
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Braford-Goldberg, Sarah R.
Caparon, Maire H.
Paston, Alan M.
Klein, Barbara K.
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APPLICATION NUMBER: US 08/192,325
TILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Abrams, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 34,547
REPERBORD/DOCKET NUMBER: C-270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-696
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: DNA (genomic)
US-08-468-609A-70
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Olins, Peter O.
Paik, Kumnan
APPLICANT: Olins, Peter C. APPLICANT: Paik, Kumnan APPLICANT: Thomas, John W.
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Best Local Similarity 50.0%
Marches 67, Conservative
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EDNESS: double
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STREET: F. CLIIX: Chicago
TITY: Chicago
TATF: Illinois
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US-08-468-569A-71/c
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APPLICANT:
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                                                                                                                                                                                                                         COUNTRY:
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                                      APPLICANT: McKearn, John P.
APPLICANT: Olins, Peter O.
APPLICANT: Palk, Xumnan
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
NUMBER OF SEQUENCES: 197
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                                                                                                                                                                            Dennis A. Bennett, G.D. Searle & Co. Corporate Patent Dept.
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parametin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,609A
FILING DATE: 06-JUN-1995
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APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-PEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
RESISTATION NUMBER: 34,547
REFERRACE/DOCKET NUMBER: C-2790/3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Braford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
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Patent No. 6030812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / MOLECULE TYPE: DNA (genomic)
US-08-468-609A-68
                         Klein, Barbara K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (314)737-6966
TELEPAX: (314)737-6972
INFORMATION FOR SEQUENCE SEQUENCE CHARACTERISTICS:
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    Easton, Alan M.
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EDNESS: double
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ADDRESSEE: Dennis A.
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RY: USA
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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US-08-468-609A-70/c
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                   APPLICANI:
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63 GGGGGGGAGGAGGAGAGCACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGC 122
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             ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co., ADDRESSEE: Corporate Patent Dept.
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...=R: US/08/446,872A
05-JUN-1995
N: 424
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Braford-Goldberg, Sarah R.
                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DAIA:
APPLICATION NUMBER: US 08/192,325
FILING DAIE: 14 FEB-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REPERENCE/DOCKET NUMBER: C-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TCPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-446-872A-68
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Klein, Barbara K.
McKearn, Jonn P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : (314)737-6986
(314)737-6972
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                                                                                                                                                                    Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: Gouble
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                                                      P. O. Box 5110
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CORRESPONDENCE ADDRESS:
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 CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                             STREET: P. C. CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                               50680
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APPLICANT:
APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (1L-
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Fusion Protein
197
                                                  ADDRESSEE: Dennis A. Bennetz, G.D. Searle & Co., ADDRESSEE: Corporate Patent Dept.
STREET: P. C. Box 5110
                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
AMME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
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06-JUN-1995
                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSIEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 68, Application US/08446872A Patent No. 6361977
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McKearn, John P.
Olins, Peter O.
Paik, Kumman
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REFERENCE/DOCKET NUMBER: C-2
TELECOMMUNICATION INFORMATION:
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Easton, Alan M.
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(314)737-6972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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EDNESS: double
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                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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Best Local Similarity
Matches 67, Conserva
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US-08-445-872A-68/C
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                                                                                                                                                            SOFTWARE STATEM TO TOO WESTER #1.05
CURRENT APPLICATION DATA:
RAPHICATION NUMBER: US/08/446,872A
FILING DATE: US-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
RAPHICATION NUMBER: US/08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bauer, S. C.
Braford-Goldberg, Saran R.
Caparon, Maire H.
Baston, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
                                                                                                                                                                                                                                                                                                                  NAME: Bencet, Dennis A.
RECISTRATION NUMBER: 34,547
REFENCE/DOCKET NUMBER: C-2790/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
INFORMATION FOR SEQ ID NO: 70: SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
3: Corporate Patent Dept. P. O. Box 5110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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                                                                                                                     Floppy disk
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STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
                                                                                                 COMPUTER READABLE FORM:
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TITLE OF INVENTION:
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Best Local Similarity
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                                                                                                                   MEDIUM TYPE:
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STREET: P.
                                                                                   60680
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 ADDRESSEE:
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COUNTRY:
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63 GGGCGGGGAGGAGGAGACACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGC 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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19.3%; Score 26.8; DB 4; Length 966;
Best Local Similarity 50.0%; Pred. No. 5.1;
Matches 67; Conservative 0; Mismatches 67; Indels
                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/446,872A FILING DATE: 06-JUN-1995 CLASSIFICATION: 424 PRIOR APPLICATION NUMBER: US/08/192,325 FILING DATE: 14-FEB-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: February 3, 2003, 21:03:28 Job time : 53.524 secs
                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Bennett, Dennis A. REGISTRANTON NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/1
TELECOMMUNICATION INPORMATION:
                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (314)737-6986
(314)737-6972
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SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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7959.555 Million cell updates/sec
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/ cgn2_6/ptodata_// pubpna/US07_PUBCOMB.seq:*
/ cgn2_6/ptodata_// pubpna/US06_NEW_PUB.seq:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Iotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396772 seqs, 224532407 residues
                                                                                                                                                                                                                                                                                                                                US-09-596-141C-3_COPY_1394_1532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                 - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum OB seq length: 2000000000
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Perfect :
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Pred. No. is the number of results predicted by chance to lave a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 1, Appli Sequence 1, Appli Sequence 320, Appli Sequence 6019, Ap Sequence 6019, Ap Sequence 30, Appli Sequence 314, Ap Sequence 314, Ap Sequence 7, Appli Sequence 17, Sepli Sequence 17, Sepli Sequence 17, Sepli Sequence 17, Sepli Sequence 17, Sepli Sequence 17, Sepli Sequence 17, Sepli
SUMMARIES	US-09-846-456-3 US-09-846-456-1 US-09-31-877-1 US-09-325-300-320 US-09-338-842A-2277 US-09-234-0938-6019 US-09-294-0938-6019 US-09-880-107-3768 US-09-880-107-3814 US-09-10-220C-7 US-09-10-220C-7 US-09-10-220C-7 US-09-10-220C-7 US-09-10-220C-7 US-09-10-20C-157-7 US-09-912-157-7 US-09-912-157-4 US-09-912-157-4 US-09-912-157-4 US-09-912-157-4 US-09-912-157-4
DB	100 110 110 110 110 100 100 100
Length	2883 3029 3029 1020 280 280 280 198265 1622 2319 2319 2318 2383 3083
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Result No.	000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

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20	-09-753-436-119	-09-867-701-255	-09-925-360-141	-39-864-761-2395	-09-864-761-1399	-09-864-761-722	-09-983-965-206	-09-919-580-49	-09-731-231A-	-09-796-692-26	S-09-796-692-68	-09-864-761-758	-09-815-242-985	-10-044-090-21	-09-867-701-875	-09-983-965-409	-09-925-299-8	-09-960-352-7	-09-876-889-28	-09-764-864-15	-13-098-841-27	-09-964-899-1	S-09-964-899-1	-09-964-899-5	-10-003-295	-09-878-574-584
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AL1GNMENTS

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APPLICANT: Fojo, Silvia
TITLE OF INVENTION: Regulatory Nucleic Acid for the ABCI Gene, Molecules Modifying
TITLE OF INVENTION: Activity and Therapeutic Uses
FILE RETERENCE: 3806-0505
CURRENT APPLICATION NUMBER: US/09/845,456
CURRENT APPLICATION ADDIE: 2001-05-02
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                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 2001-05-02
PRIOR PILING DATE: 2001-05-02
PRIOR FILING DATE: 2000-05-02
NUMBER 05-50
SOGIWARR: CS-50-50
                                      Sequence 3, Application US/09846456 Patent No. US20020146792A1
                                                                                                                                                                        Denefle, Patrice
Buverger, Nicolas
Brewer, Bryan
Remaley, Alan
Fojo, Silvia
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                                                                                                               Praces, Catherine
Lemoine, Cendrine
Naudin, Laurent
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Best Local Similarity 99.3
Matches 138; Conservative
                                                                                             APPLICANT: Rosier, Marie
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US-09-846-456-3
                                                                             GENERAL INFORMATION
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RESULT 1
US-09-846-456-3
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APPLICANT:
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NAME/KEY: primer_bind
LOCATION: 14952..5512
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer_bind
LOCATION: 15460..15482
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INFORMATION: 17-41.rp complement
                                                       GOCATION: 10946..12946
OTHER INFORMATION: 5'regulatory region
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OTHER INFORMATION: 20-828.rp c
NAME/KEY: prinser_bind
LOCATION: 12029.12050
OTHER INFORMATION: 17-42.pu
NAME/KEY: primer_bind
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OTHER INFORMATION: 20-853-415
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NAME/KEY: allele
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OTHER INFORMATION: 20-842-115
NAME/KEY: allele
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OTHER INFORMATION: 20-841.rp
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OTHER INFORMATION: 20-842.pu
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OTHER INFORMATION: 20-828.pu
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OTHER INFORMATION: exon 3
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OTHER INFORMATION: exon 4
                                                                                                                                          OTHER INFORMATION: exon 1
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LOCATION: 45328..45347
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LOCATION: 42070..42090
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LOCATION: 15969..17969
  Homo sapiens
                                      NAME/KEY: misc_feature
LOCATION: 10946..12946
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LOCATION: 42572..42591
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LOCATION: 929..949
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LOCATION: 45863..4588:
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LOCATION: 15241
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LOCATION: 1239
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LOCATION: 12347
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  ORGANISM:
                                                                                                                       LOCATION:
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APPLICANT: Remaley, Alan
APPLICANT: Fojo, Silvia
TITLE OF INVENTION: Regulatory Nucleic Acid for the ABCI Gene, Molecules Modifying IT
IITLE OF INVENTION: Activity and Therapeutic Uses
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APPLICANT: Sougheleret, Lydie
APPLICANT: Ebbers-Reed, Dana
APPLICANT: Ebbers-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89.US3.REG
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Pred. No. 1.2e-36;
0; Mismatches 1; Indels
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APPLICANT: Bour, Barbara
Bibain, Bernard
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
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CURRENT FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent.pm
SSQ ID NO 1
LENOTH: 81001
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/846,456 CURRENT FILLING DATE: 2001-05-02
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PRIOR PLICATION NUMBER: US 60/201,280
PRIOR FILING DATE: 2000-05-02
NUMBER OS SEQ ID NGS: 20
SOFTWARE: Patentin version 3.0
FIGURE OF THE NOTE OF THE OF THE OF THE OF THE OF THE OF T
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Patent No. US20020042049A1
GENERAL INFORMATION:
APPLICANT: Yen, Frances
                                                                                                                    Sequence 1, Application US/09846456 Patent No. US20020146792A1
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2855 GCCGAAICTATAAAAGGAA 2873
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Duverger, Nicolas
                                                                                                                                                                                  APPLICANT: Rosier, Marie APPLICANT: Prades, Catherine
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Naudin, Laurent
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CRGANISM: Homo sapiens
US-09-846-456-1
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Best Local Similarity
Matches 138; Conserv
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US-09-751-877-1/C
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APPLICANT:
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Db 17479 GGGCTGCTGCTCCTCGTCGTCGCGCTGATGGGCCCGGAACAGGTGAGCAGGCGCAGGCGG 17420
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OTHER INFORMATION: 20-928-311.mis
NAME/KEY: Primer_bind
LOCATION: 1240.1258

OTHER INFORMATION: 20-828-311.mis complement
NAME/KEY: Primer_bind
COCATION: 12238...12346
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: Primer_bind
LOCATION: 12348...1356
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: Primer_bind
LOCATION: 15242...15240
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: Primer_bind
LOCATION: 15342...15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: Primer_bind
LOCATION: 42199...4227
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: Primer_bind
LOCATION: 4523...6540
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: Primer_bind
LOCATION: 4523...6541
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: Primer_bind
COTHER INFORMATION: 20-841-149.mis
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LOCATION: 77039..77057
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OTHER INFORMATION: 20-853.rp complement
NAME/KEY: primer_bind
LOCATION: 1220..1236
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NAME/KEY: misc_binding
LOCATTON: 42206. 42230
OTHER INFORMATION: 26-841-149.probe
LOCATION: 45430..45454
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OTHER INFORMATION: 20-828-311.probe
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LOCATION: 12335. .12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc_binding
LOCATION: 15229. .15253
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LOCATION: 77059..77077
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Best Local Similarity
Matches 48; Conserva
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US-09-925-300-320/c
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GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Harper, Jeff
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPING DATE: 2001-08-24
CURRENT FILING DATE: 2001-08-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 21.3%; Score 29.6; DB 10; Length 1756; Sest Local Similarity 60.3%; Pred. No. 1.2; Matches 47; Conservative 1; Mismatches 30; Indels 0;
                                                                       APPLICANT: Steve Ruben,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies;
FILLE REPERENCE: PA1.01
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT PILING DATE: 2001-08*.20
PRIOR APPLICATION NUMBER: PCT/US00/05986
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOOTWARE: Patentin Ver. 2.0
SEQ ID NO 3.20
LENGTH: 1756
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PRIOR APPLICATION NURBER: US 50/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-22
NUMBER: US 50/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER: CS SEQ ID NOS: 5379
LENGTH: 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1733)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1750)
COTHER INFORMATION: n equals a,t,g, or c
US-09-925-330-320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-936-842A-2277/c; Sequence 2277, Application US/09938842A; Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1718)
OTHER INFORMATION: : equals a,t,g, or
NAME/KEY: misc feature
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ORGANISM: Arabidopsis thaliana
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Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
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APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
TITLE OF A-0.02 CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT APPLICATION NUMBER: 2002-01-69
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 30
LENGIH: 1466
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                                                                                             PRIOR AFFLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
PRIOR FLING DATE: 2000-05-01
PRIOR FLING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-20
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-04
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-08-07
PRIOR PRIOR FILING DATE: 2000-08-07
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PRIOR PRIOR PRIOR DATE: 2000-08-07
PRIOR PRIOR DATE: 2000-08-07
PRIOR PRIOR DATE: 2000-08-07
PRIOR PRIOR PRIOR DATE: 2000-08-07
PRIOR APPLICATION NUMBER: 60/190,479 PRIOR FILING DATE: 2000-03-17 PRIOR APPLICATION NUMBER: 60/200,545
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LOCATION: (383)
OTHER INFORMATION: n=A,I,C or G
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OTHER INFORMATION: n=A,T,C or
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Best Local Similarity 53.22
Lohas 58; Conservative
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ORGANISM: Homo sapiens
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LOCATION: (341)
OTHER INFORMATION:
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NAME/KEY: unsure
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Publication No. US20020198362A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INTERIOR OF US OF
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APPLICANT: Lalgudi, Ragiunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradloy, K.
TITLE OF INVENTION: POLYNOCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
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                                                                                                                                                                                                                                                                                                                     64 GGCGGGGAGGAGGAGGAGCACAGGCTTTGACCGAIAGTAACCTCTGCGCTCGGTGCAGCC 123
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                                                                                                                                                          4 OCCOGGCTCCACGTGCTTTCTGCTGACTGACTGAACTACATAAACAGAGGCCGGGAACGG 63
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        Score 28.6; DB 9; Length 975; Pred. No. 2.1;
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OTHER INFORMATION: Incyte ID No. US20010051335A1 700382861H1
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                                                                                 59; Indels
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63.6%; Pred. No. 3.1;
tive 0; Mismatches 24;
                                                                                     0; Mismatches
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
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        20.6%;
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                                                                                     64; Conservative
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        Query Match
Best Local Similarity
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Best Local Similarity
Matches 42; Conserv
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ORGANISM: Zea mays
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US-09-294-093B-6019
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US-09-796-692-6574
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562 IAA 560
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SEQ ID NO 6019
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LENGTH: 198285
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                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                19.6%; Score 27.2; DB 16; Length 66109; 56.0%; Pred. No. 24; Live 0; Mismatches 68; Indels 0;
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APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Jwe
APPLICANT: Scherf, Jwe
APPLICANT: Gene LogLo, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer; FILE OF INVENTION: Gene Expression Profiles in Liver Cancer; FILE OF INVENTION: Gene Expression Profiles in Liver Cancer; PRISERENCE: 44921-5028-Wo
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/221,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
                                                                                        Length 1465;
NAME/KSY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 4843159CB1
                                                                                                                                      Indels
                                                                                   Match 19.7%; Score 27.4; DB 12: Local Similarity 59.7%; Prec. No. 6.1; es 46; Conservative 0; Mismatches 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1)...(66109)
; CTHER INFORMATION: n = a or c or g or t
US-09-880-107-3768
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Patent No. US20020142981A1
GENERAL INFORMATION:
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APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35031 CCCAAAGGAAGACAAG 35046
                                                                                                                                                                                                                                                                             123 CGAATCTAIAAAGGAA 139
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                                                                                                                                                                                                                                                                                                                            38 CTTAAAAAAAAAAA 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 68; Conserval
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US-09-880-107-3768
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    ; NAME/KEY: mi
; OTHER INFORM
US-10-044-090-30
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                                                                                             Query Match
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Matches
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Db 110760 ATGGGGCCTGAGAAGAAATGCAAGTTAGGACAAAAGAGTTACAGGTGAGGGTT 110819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 198285;
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US-09-880-107-3814
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TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REFERENCE: 44921-5028-WO CURRENT APPLICATION NUMBER: US/39/880,107 CURRENT FILING DATE: 2001-06-14 PRIOR APPLICATION NUMBER: US 60/211,379 PRIOR FILING DATE: 2000-06-14 PRIOR APPLICATION NUMBER: US 60/237,054 PRIOR FILING DATE: 2000-06-14 PRIOR FILING DATE: 2000-10-02 NUMBER OF SEQ ID NOS: 3950 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 3314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: ONE POST OFFICE SQUARE CITY: BOSTON
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FILING DATE: 24-Jul-1997
CLASSIFICATION: <Unknown>
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ilarity 50.0%; Pred. No. 35;
Conservative 0; Mismatches
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COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
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Pang, Kevin
Jin, Ping
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TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08900220C Patent No. US20020045206Al GENERAL INFORMATION: ApplicaNT: Miso. Ningning
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Les 68; Conserva
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GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
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PRIOR FILING DATE:
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APPLICANT: Wang, Elizabeth
APPLICANT: Wang, Elizabeth
TITLE OF INVENION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE
TITLE OF INVENION: POLYPEPTIDES, AND FCRMULATIONS AND USES RELATED THERETO
FILE REPERENCE: ONV-031.02
FURENT APPLICATION NUMBER: US/09/151,999
CURRENT FILING DATE: 1998-06-11
EARLIER APPLICATION NUMBER: 08/955,552
EARLIER FILING DATE: 1997-10-20
NUMBER OF SEQ ID NOS: 28
SOTUMARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                               Score 27; DB 8; Length 1622;
Pred. No. 8.6;
0; Mismatches 60; Indels
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US-05-874-503-17
Sequence 17, Application US/09374503
Parent No. US20020177188A1
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LENGTH: 1622 base pairs
TYPE: nucleic acid
STRANJEDNESS: both
                                                                                                                                                                                                                               19.4%;
                                                                                                                       NAME/KEY: CDS
LOCATION: 51..1283
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                                                                           MOLECULE TYPE: CDNA
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US-09-151-999-7
                                                                                                                                                                                                                                                     Best Local Similarity
Matches 53; Conserva
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|1346 GGA 1348
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                                                                                                          FEATURE
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Best Local S
Matches 63
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APPLICANT: Yansura, Daniel
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381RIC1P3 (US)
CURRENT APPLICATION NUMBER: US/09/874,503
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/253,646
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PRIOR APPLICATION NUMBER: US PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US PCT/USC0/30873
PRIOR FILING DATE: 2000-11-10
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2001-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/244,C72
PRIOR PILIAG DATE: 2000-10-26
PRIOR PILIAG DATE: 2000-10-24
PRIOR FILIAGION NUMBER: US 60/175,481
PRIOR FILIAGION NUMBER: US 60/175,481
PRIOR PAPLICATION NUMBER: US 60/175,401
PRIOR APPLICATION NUMBER: US 60/1907
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PRIOR APPLICATION NUMBER: US 60/085,579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: US 99/854,208
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-20
PRIOR FILING DATE: 2001-05-20
PRIOR APPLICATION NUMBER: US 09/854,280
PRIOR APPLICATION NUMBER: US 09/816,744
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TSB 60/113,621
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PRIOR FILING DATE: 2000/08-22
PRIOR APPLICATION NUMBER: US 09/386,142
PRIOR FILING DATE: 1995-08-25
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JECATION NUMBER: US 60/172,396
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LICATION NUMBER: US 60/138,387
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PRIOR APPLICATION NUMBER: US 09/747,259
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PRIOR APPLICATION NUMBER: US 09/311,832
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                                                                               Grimaldi, J. Christopher
                                                                                                                                                                                                                                      Starovasnik, Melissa A
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Williams, P. Mickey
                                                                                                                                                                                                                                                                    VanLockeren, Menno
                                                                                                                                   Li,Hanzhong
Hilian,Kenneth J.
Hymowitz,Sarah G.
                                                                                                        Gurney, Austin L.
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                                                         Godowski, Paul J.
                                                                                                                                                                                                                                                                                          Vandlen, Richard
Fong, Sherman
Goddard, Audrey
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PRIOR FILING DAIE: 1999-06
PRIOR APPLICATION NUMBER:
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APPLICATION NUMBER:
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                       Wood, William
                                                                                                                                                                                                                Tumas,Daniel
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2006-06-02
IMBER: PCT/US00/23328
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PRIOR APPLICATION NUMBER: PCT/US00/32678
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PRIOR FILING DATE: 2000-03-21
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PRIOR APPLICATION NUMBER: PCI/US00/30873
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PRIOR APPLICATION NUMBER: PCT/US99/31274
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PRIOR APPLICATION NUMBER: PCT/US99/10733
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                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/19107
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-06-22
PRIOR PRIOR OFFICATION NUMBER: 60/242877
PRIOR APPLICATION NUMBER: 60/244672
PRIOR APPLICATION NUMBER: 60/24472
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 1090-05-14
PRIOR APPLICATION NUMBER: 60/253646
PRIOR PLING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/381183
PRIOR APPLICATION NUMBER: 09/38018
PRIOR PILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 09/38018
PRIOR APPLICATION NUMBER: 09/38018
PRIOR PILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/38018
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PRICE FILING DATE: 2000-08-22
PRIOR PLICATION NUMBER: 09/747259
PRIOR PELICATION NUMBER: 09/747259
PRIOR PLING DATE: 2000-13-20
PRIOR APPLICATION NUMBER: 09/864208
PRIOR PELING DATE: 2001-03-10
PRIOR FILING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
PRIOR PLING DATE: 2001-05-10
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/874503
PRIOR APPLICATION NUMBER: 09/874503
PRIOR FILING DATE: 2001-05-10
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PRIOR FILING DATE: 2001-07-18
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PRIOR APPLICATION NUMBER: 09/918585
PRIOR PLING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/929404
PRIOR FILING DATE: 2001-08-13
PRIOR PRILING DATE: 2001-08-13
PRIOR PRILING THE: 2001-08-16
PRIOR APPLICATION NUMBER: 09/931836
PRIOR APPLICATION NUMBER: 09/931836
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APPLICATION NUMBER: 60/191007
FILING DATE: 2000-03-21
APPLICATION NUMBER: 60/213807
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FILING DATE: 2001-0.
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                                                                FILING DATE: 1999-06
APPLICATION NUMBER:
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IITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381R1C1P4(US)
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                                                             PRIOR APPLICATION NUMBER: US PUL/USOU/15204
PRIOR APPLICATION NUMBER: US PUL/USOU/15204
PRIOR PILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-03-12
PRIOR PILING DATE: 2000-03-12
PRIOR APPLICATION NUMBER: US PCT/USOC/05841
PRIOR APPLICATION NUMBER: US PCT/USOC/05601
PRIOR APPLICATION NUMBER: US PCT/USOC/04341
PRIOR APPLICATION NUMBER: US PCT/USOS/04/341
PRIOR PILING DATE: 2000-03-01
PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US PCT/USO9/10733
PRIOR PAPLICATION NUMBER: US PCT/USO9/05C28
PRIOR PRILING DATE: 1999-05-14
PRIOR PRILING DATE: 1999-03-08
NUMBER: OF SEO ID NOS: 39
PRIOR APPLICATION NUMBER: US PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
                            PRIOR FILING DATE: 2000-08-24
PRIOR APPLICALION NUMBER: US PCT/US00/15264
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CURRENT FILING DATE: 2002-10-30
PRICA APPLICATION NUMBER: 60/085579
PRICR FILING DATE: 1998-05-15
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PRIOR PELLING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR PELLING DATE: 1999-04-21
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Goddard, Audrey
Godowski, Paul L.
Grimaldi, J.Christopher
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Starovasnik, Melissa.
VanLookeren, Menno
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Li, Hanzhong
Hillan, Kenneth J.
Hymcwitz, Sarah
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Williams, P.Mickey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
; ORGANISM: Homo Sapien
US-09-874-503-17
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Best Local Similarity
Matches 45; Conserv
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Publication No.
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LENGTH: 2319
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PCT/US00/23328

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PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                      Length 2319;
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                                                                                                                                                                                                                                         Score 27; DB 9;
Pred. No. 9.7;
                                                                                                                                                                                                                                                                                   0; Mismatches
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PRIOR FILING DATE: 1399-05.14
PRIOR FILING DATE: 1399-12.23
PRIOR FILING DATE: 1999-12.23
PRIOR FILING DATE: 1999-12.23
PRIOR APPLICATION NUMBER: PCT/US99/31274
PRIOR PELICATION NUMBER: OS 05/175,481
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
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PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-21
PRIOR PRICHAGININ NUMBER: PCT/USOU/07532
PRIOR PELING DATE: 2000-03-21
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US 60/213,087
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US 60/213,087
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 201-06-20
PRIOR APPLICATION NUMBER: PCTJUS01/21056
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/09747259 Publication No. US20030098815A1 GENERAL INFORMATION:
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Grimaldi,Christopher
Gurney,Austin
                                                                                                                                                                                                                                           19.48;
60.08;
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Wood, William
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Fong, Sherman
Goddard, Audrey
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Hillan, Kenneth
Tumas, Daniel
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Watanabe, Colin
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                                                                                                                                                                                 ; ORGANISM: Homo Sapien
US-10-030-157-17
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Best Local Similarity
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US-09-747-259-17
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## PRIOR APPLICATION NUMBER: US 60/242,837

| PRIOR APPLICATION NUMBER: US 60/242,837
| PRIOR PILING DATE: 2000-10-24
| PRIOR PILING DATE: 2000-11-20
| PRIOR PILING DATE: 2000-11-20
| PRIOR FILING DATE: 2000-12-01
| PRIOR FEDRUARY 3, 2003, 16:37:53
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                             2054540 segs, 14551402878 residues
                                                                                                                                    US-09-596-141C-3_COPY_1394_1643
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Listing first 45 summaries
                                                     nicleic search, using sw model
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is the number of results predicted by chance to have a . N Pred.

AF275948 Homo sapi AF285623 Homo sapi AF287262 Homo sapi AC021345 Homo sapi AE258627 Homo sapi Mus muscu 3 Mus muscu AX351032 Sequence AX351032 Sequence AK024328 Homo sapi AK022254 Homo sapi AC125837 Rattus no Homo sapi Human DNA Homo sapi Sequence Seguence Sednence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description AL807243 M. AF287263 N AL359182 | AC012230 | AX351029 AF275948 AJ252201 AX092589 AX351031 AX050894 SUMMARIES AX092589 AX351029 AF275948 AF25862351 AL807243 AF287263 AC021246 AL359182 AC012230 AF287262 AC021246 AC021345 AF258627 AX351031 AX060894 AC125837 AX351032 DB 100.0 10 Length Query Match 250 248.4 248.4 246.8 246.8 226.8 173 157.4 132.8 132.8 Score 98 Result 02

ALIGNMENTS

AC10581,
AX182501 Sequencon AC118464 Homo sapi
AC011429 Homo sapi
AC023861 Homo sapi
AC023861 Mouse DNA

AX060719 Sequence AX060721 Sequence AX060808 Sequence AX060900 Sequence AC122157 Rattus no L27081 Rat melanoc

AX060/22 AX660892 Sequence AF285167 Homo sapi

AX060892 AF285167 AX060719 AX060721

75 75 67 67 60 60 60 80 80

AX060898 AX060900

90

RATMC5R

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150542 129025 38796

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Sequence Sequence Sequence

AX127831 AX139816 AX060713

AK022254 AX127831 AX139618 AX060713

AK024328

89.4 89

AL121772 Human DNA AC091390 Homo sapi AF030453 Homo sapi AC097603 Rattus no AX092823 Seguence

ACC97603 J AXC92823 S AC105817 J

AC097603 AX092823 AC105817 AX182501 AC118464

AC011429 AC023861

14.5 122557 14.5 191397 14.5 201635 14.5 220087

PRI 10-APR-2001 HSA252201 1167 bp DNA linear PRI 1 Homo sapiens partial ABC-1 gene for ATP-binding cassette transporter-1, 5'GTR and promoter region. ABC-1 gene; ATP-binding cassette transporter-1; promoter. AJ252201 AJ252201.1 GI:12053757 human. HSA252201 LOCUS DEFINITION ORGANISM ACCESSION AUTHORS REFERENCE XEYWORDS SOURCE VERSION

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Location/Qualifiers
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The zinc finger protein 202 (ZNF202) is a transcriptional repressor of ATP binding cassette transporter Ai (ABCA1) and ABCG1 gene expression and a modulator of cellular lipid efflux J. Biol. Chem. 276 (15), 12427-12433 (2001)
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Submitted (05-JaN-2000) Forsch-Oezcueruemez M.K., Institute for Clinical Chemistry, University of Regensburg,
Frants-Josef-Strauss-Allee 11, 93042 Regensburg, GERMANY
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                         /function="cholesterol efflux regulatory protein"
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/gene="ABC-1"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, 1
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AX060715.1 GI:12406104
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1643)

Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.

Atp binding cassette transporter protein abol polypeptides

Patent: WO 00799971-A 3 28-DEC-2000;

CV THERAPSUTICS, INC. (US)

Location/Qualifiers
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Llarity 100.0%; Pred. No. 6.8e-58;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 6.8e-58;
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413 c 457 g 40
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contig of 853 bp in length

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contig of 851 bp in length
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37128: contig of 872 bp in length
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contig of 841 bp in length
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contig of 851 bp in
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14241: contig of 861 bp
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9: gap of
9430: contig of
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18041: cont
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21865: con+
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29492: cont
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__i gap of
36156: _
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31410: cont
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33312: cont
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5640: con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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-1N10, LOW-PASS SEQUENCE SAMPLING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L2512
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872 1834: contig of 863 bp in length

1935 1934: gap of 100 bp

1935 2904: gap of 100 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome, clone RP11-1N10
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                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens clone RP11-1N10,
AC021246
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KEYWORDS VERSION

SOURCE

RESULT 4 AC021246 LOCUS

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PRI 11-JAN-2002

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AL359182 BA linear PRI 11-JAN-2007
Human DNA sequence from clone RPI1-217B7 on chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (11-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 15, 2002 This sequence version replaced gi:18121468.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                       Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.chori.org/bacpac/home.htm
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TITLE
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contig of 867 bp in length
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24: gap of 100 bp
43776: contig of 852 bp
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85: gap of 100 bp
50440: contig of 855 bp
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41913:
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48551: _
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Best Local Similarity
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variation amortation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with this sequence was finished as follows unless otherwise noted: all regions were either double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following absendations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBJ; Sw., SWISSPROT; Tr., TREMBL; WP., MORMPEPP, Information on the WORMPEPP that was not the workers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMPORTANT: This sequence is not the entire insert of clone RP11-21787 it may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true right end of clone RP11-21737 is at 96717 in this sequence. The true left end of clone RP11-127810 is at 72980 in this sequence. The true right end of clone RP11-31320 is at 2000 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sarger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/HGP/Chr9
RPI1-217B7 is from the library RPCI-i1.1 constructed by the group
of Pieter de Jong. For further details see
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/db_xref="taxon:9606"
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Indels

Db 41406 GGGCCCGGCTCCACGTGCTTTCTGCTGAGTGACTACATAAACAGAGGCCGGGAA 41455 61 CGGGCCGGGGAGGAGGAGCACGCTTTGACCGATAGTAACTCTGCGCTCGGTGCA 120

0; Mismatches

Conservative

250;

Matches

50

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(Dassel to 175064)

Bairen, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Bairan, B., Enton, L., Rushaum, C., Lander, R., Bouslavkiy, L., Boukhgalter, B., Cooke, P., Castle, A., Colangeio, M., Collins, S., Collymore, A., Cooke, P., Deareliano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzBugh, W., Forrest, C., Funke, R., Gaqe, D., Galagan, J., Garafran, R., Hagos, B., Hadord, A., Eorto, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Kielis, J., Lehoccky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughilh, J., Meldrim, J., Morrow, J., Naylor, J., Nana, C., Roy, A., Santos, R., Severy, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
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Homo sapiens cione RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered
pieces.
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Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 175064)
                                                                                                                                                                                                                                                                     derived from a single pUC clone. Restriction digest data confirm the assembly."
                                                                                                                                                                                                                                                                                                                                                                 /note="Sequence from reads from a short insert library derived from a single pUC close. Restriction digest data confirm the assembly assembly 27673 a 21136 c 20380 g 27526 t.
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                                                                                                                                                                             /note="Sequence from overlapping close RPI1-122F10 (AC026643). Assembly confirmed by restriction digest."
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/note="Sequence from reads from a short insert library
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                                                                                           institute, of Heath, National Heart, Lung and Blood Institute, Bethesda, MD 20892, USA."
                                                                               /note="Sequence from AF275948 sequenced by National
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 250; DB 9;
100.0%; Pred. No. 5.2e-58;
tive 0; Mismatches 0;
/clone="RP11-217B7"
/clone_lib="RPCI-11.1"
3238. .3278
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Somo sapiens, clone RPII-1MIC
Unpublished
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                                                                                                                                                                                                            (AC026643)
92050. 921
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Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo.A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (21-0CT-1999) Whitehead Institute/MII Center for Genome Research, 320 Charles Street, Cambridge, NA 02141, USA OI Apr 22, 2000 this sequence version replaced $1:6454033.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemistry: Dye-terminator Big Dye; 1004 of reads Assembly program: Phrap: version 0.960731 consensus quality: 11751 bases at least Q40 consensus quality: 145749 bases at least Q40 consensus quality: 145749 bases at least Q20 consensus quality: 160940 bases at least Q20 consensus quality: 160940 bases at least Q20 consensus quality: 160940 bases at least Q20 consert size: 185000; aqarose-fp ceality coverage: 2.9 in Q20 bases; agarose-fp quality coverage: 3.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
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22688 25707: contig of 3020 bp in length
25708 25807: gap of 100 bp
28185 28284: contig of 2377 bp in length
28185 28284: gap of 100 bp
28285 31338: contig of 3054 bp in length
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------ Summary Statistics
Sequencing vector: M13; M77815;
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9786: gap of 10
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1 (bases 1 to 18399)

Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M. Compositions and methods for modulating fidl cholesterol and triglyceride levels

Patent: WO 0115676-A 1 08-WAR-2001;
University of British Columbia (CA); Xenon Genetics Inc. (CA)

1. 183999
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/note="assembly_fragment"
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axequence 1 from Patent W00115676.

AX092589

AX092589.1 GI:13444647
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71559. .76888
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19 45548: gap of 100 bp

48116: contig of 2568 bp in length

17 52618: contig of 4402 bp in length

19 5218: gap of 100 bp

19 56592: contig of 3874 bp in length

31 5692: gap of 100 bp

32 5692: contig of 2943 bp in length

33 59635: contig of 2943 bp in length
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175064: contig of 17573 bp in length
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45592 157391: contig of 11800 bp in length
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5125 bp in length
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6062 bp in length
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76888: contig of 5330 bp in length
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1. .1003
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                                                                                                                                            28631 GGGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAACAGAGGCCGGGAA 28690
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/organism="Homo sapiens"
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37944 c 4117C g 54950
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1 (bases 1 to 149034)
Santamarina-Folo, B., Peterson, K., Knapper, C., Qiu, Y., Freeman, L., Cheng, J.F., Osorio, J., Remaley, A., Yang, X.P., Haudenschid, C., Praces, C., Chimini, G., Blackmon, E., Francois, T., Duverger, N., Rubin, E.M., Resier, M., Denefle, P., Fredrickson, D.S. and Brewer, H.B.
                                                                                                                                                                                                                                                                                                     Complete genomic sequence of the human ABCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter Proc. Nati. Acad. Sci. J.S.A. 97 (14), 7987-7992 (2000)
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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Santamarino-Fojo,S., Peterson,K.M., Knapper,C.L., Freeman,J.A.,
Remaley,A.T., Yang,X.-P., Haudenschild,C.C., Blackmon,E.E.,
Francois,T.L. and Brewer,H.B. Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-JUN-2000) Molecular Disease Branch, National Institutes of Heath, National Heart, Lung and Blood Institute, Betnesda, MD 20892, USA
Location/Qualifiers
1. 149034
/ Organism="Homo sapiens"
/ db_xref="taxon:9606"
/ db_xref="taxon:9606"
/ gene="ABCA1"
    linear
              Homo sapiens ABCAl (ABCAl) gene, complete cds. AF275948
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5563. 5839
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NRFGDGYJJVVRJAGSNPDLKPVQDFFGLAFPGSVXKBKHRNMLGYQLPSSLSSLARJ
FSJLSQSKKRLJJEDYSVSQTJLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLT
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DILQDLJGRNISDYLVKTYVQIIAKSLKNKIWYNFFRYGGFSLGVSNTQALPPSQEVN
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ELDGGGGDUDILEIKRLTKIRKRKRRANDRLCVGIPPGECFELGVVRGKSSTFKM
LTCDFTVFRCDAFLKKLSLISNIHEYVLQMAVVCPQDATTELLTGGREVVEFFALLRCV
PEKSVGKVGEWAIRKLGLVKYGEKYACNYSGCNKRKLSTAMALLGGPPVVFLDEPTTG
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NLSLPKSTVDKMLRADVILHKVFLQGYQLHLISLCNGSKSEEMIQLGDQEVSELCGLP
REKLAAAERVLRSNMDILKPILRTLNSTSPF?SKELABATKTLLHSLGTLAQELFSMR
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EQGIGVQWDNLFESPVEEDGFYLFTSVSMKLFDTFLYGVMTWYIEAVFPGQYGIPRPW
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QNLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEKEVKAEMEQMALDVGLPSSKLKSKT
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TYVLPY BAAKEGAFVELFHEIDDRLSBLGISSYGISETTILEEIFLKVAEESGVDAETS
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LQPWMYNBQYTFVSNDAPEDIGTLELLNALTKDPGFGTRCMEGNPIPDTPCQAGEEW
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GGNGTBEDAETFYDNSTTPYCNDLMKNLESSPISRIIMKALKPLIVGKILYTPDTPAT
RQVMARVNKTFQELAVFHDLECMWEBLSPKIWTFMENSQEMDLVFMLLDSRDNDEWE
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FSWFISSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFVFLSVFAVVTILQCFLISTLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MACWPQLRLLLWKNLTFRRQTCQLLLEVAWPLF1FLILISVRL
SYPPYEQHECHFPNKAMPSAGTLPWVQG11CNANNPCFRYPTPGEAPGVVGNFNKSIV
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101048. :101169,104152. :104328,117287. :117379,
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Qiu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
Submission
Submitted (13.0ff-2000) Genome Science Department, Lawrence
Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="ATP-binding cassette 1 sub-family A member 1" 33931. .34151
                                                                                                                                                                                     181 TGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGG 240
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                                                                GCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCGTAATTGCGAGGGAGAGTGAG 180
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1 (bases 1 to 201144)
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REFERENCE
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Homo sapiens ATP binding cassette transporter 1 (ABCA1) gene,
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                                                                                                                                                GCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCGTAATTGCGAGGGAGTGAG 180
                                                                                    Sequence update by submitter
On Jun 23, 2000 this sequence version replaced gi:7769713.
Location/Qualifiers
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99.28;
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Best Local Similarity 99.29
Matches 248; Conservative
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Homo sapiens.
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/number=7 117287117379 /gene="ABCAL"	/number=8 122329. 122569 /gene="ABCA1"	/number=9 125285. 125424 /gene="ABCA1"	/number=10 125754125870 /gene="ABCA1"	/number=11 130079130276 /qene="ABCA1"	/number=12 131023131228 /gene="ABCA1"	/number=13 131749131925 /gene="ABCA1" /www.how=1	/.umber=14 133768 /gene="ABCA1" /number=15	135677135898 /gene="ABCA1"	/.umiber_10 136959137163 /gene="ABCA1"	/number=17 138268138381 /qene="ABCA1"	/number=18 140179140350	/gene="ASCAL" /number=19 141340141471	1 2	/gen="42919 /gen="61"	/bumber=zl 143123143260 /gene="ABCA1"	/number=22 143963144183 /qene="ABCA1"	/number=23 145441145513 /gene="ABGA1"	/number=24 146657146859	/gene=_ ABCA1 /number=25 148527148575 /qene="ABCA1"	/number=26 148771148884	/gene= AbcAr /number=27 150286150428 //occommonstratin	/gene="AbcAl /number=28 152078, 15202 /gene="AbcAl"	/yene= R2CA1 /number=20 153438153536 /cene="A3CA1"	/pumber=30 156568156757 /gene="ABCA1"
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122329122569,125285125424,125754125870, 130079130276,131023131228,131749131925,	133708. 1333930,133957; 130303,1345. 138268. 138391,140179. 140350,141340. 144471, 14277. 142919,141123. 143360,143963. 144183, 145441. 145512,146657. 146859,148577. 148575,	148771. 148884,159280. 150428,152078. 155202, 154488. 155358,156568. 155737,158278. 158372, 159682. 159744,166837. 160942,162417. 162491,	163013. 163182,164413. 164590,166589. 166703, 168118. 165959,168905. 168628,1689715. 156944, 176109. 1767017. 171079,171099,171987. 1772093,	174448 174589,174961 175095,176039 176142, 17625. 175717,177376 177619,178560 178700)	/gene= Abcal /codon_start=1 /product="ATP-binding cassette 1 sub-family A member 1" /profein id="AAK43526.1"	<pre>/db_xref="c1:13876613" /translation="MACWPQLRLLLWKNLIFRRQTCQLLLEVANPLFIFLILISVRL SYPPYEQHECHPPNKAMPSAGTLPWVGGITCNANNPCFRYPTPGEAPGYVGNFNKSIY</pre>	ARLESDARRLLLYSQKDTSMKDMRKVLRTLQQIKKSSSNIKLQDFLYDNETFSGFYH NISLPKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSBBMTOLGDQBVSELGGLP KEKLAAASTVULKSNMDILKPILKTINSTSPPPSKELAEATKTLLHSLGTLAQELFSKR	SWSDMRQEVMETINVBNSSSSTYLYRYRYKTYCHTEUGELTALSLUMT ELDMNITARLE GGWGTEDZAZIFYDNSTTPYCNDLAKNLESSPLSATIWKALKPLIVGKILYTPDTPAT ROYMAEVNKTYQELAYTHOLEGOWEELSPKIWTFMBNSQEMDLVRMLLDSRDNDHFWE	QOLDGIDMTAQDIVAFIZARHEDDVÖSSNGSYYTWRZAFNETNYGAIRYISRFWECVNÜN KLEPIATEVMIINKSMELLDERKFWAGAIVFTGITTGGIELPHYKYKIRMDIONVERT NKIRNGYWDPGRPRADPFEDMAYVWGGRAYLODVVEGAIIRVITGITEKKIGYVÄQQMPY	PCYVDDIFLRVMSRSMPLFMILAWIYSVAVIIKGIVYEKEARLKETMRIMGLDNSILM PCYVDDIFLRVMSRLAMILAWILLPYSDFSVYFVELEVELDGCELTSTLE PSYFISSLILDLUSPAGELLVVILKIGNIT GYARANY TAGGELGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	SKANLARAKGGALITIFILISHET ULCVANQISTVORT ILLIKARASLOSTVASIONASTALI EQGIGVONDULLFESPVEBDGFNUTISVSMALENTFIZGVANTKYTEAVEPGOYGIPRPP YPPCTKSYWFGBESBERSERSPSOKKATSBICMBEBPTHLKLGVSTQNLVKVYRDGMKV	AVDGLALNFYEGQITSFLGHNGAGKTTTMSILFGLFPPTSGTAYILGKDIREBMSTIR QNLGVCPPHVLFPDMIYVEBHTMRTFAAAGGISKKHVAARABQAALDVOLSSKAKKK GAN GANAADAT AVVGGSTAYUTTIPPTAAAGADAGABTAHLIAVRYGTTILST	HANDEADVIGDETA I SHGKLCYGSSLFIKNOLGTGYYLTLUKKDVESSLSSCRNSS STVSYLKKEDSVSQSSSDAGLGSDHESDTLTTDVSAISNLIRKHVSBARLVEDIGHEL	TYVLPYBAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEEFFLKVAEESGVDAETS DGTLPARRNRRAFGDKQSCLRPFTEDDAADPNDSDIDPESREIDLLSGMDGKGSYQVK	GWKLIQOQFVALLMKRLLIARRSRKGFFAQIVLPAVPVCTAIVPSLIYPPFGKYPSLE LOPMAYNOQYTPVSNADAPBDTGTLELIAALTKDFGFGTRCMEGNPIPDTPCQAGEBEW THA BUDOWT MAY DONGWAWAND SPACHORSKINKIKKMIPVCPPGAGGIPPPOKKUNTA	DIAGOLIGERIES DE VETTE PROFESSOR DE LE CONTROL DE LA CONTROL DE PEQUEN DE L'AGRESIA CONTROL DE PEQUEN DE L'AGRES PROFESSOR NO VETTE DE L'AGRES PROFESSOR NO VETTE DE L'AGRES PROFESSOR NO VETTE DE L'AGRES DE PENDENCE PROFESSOR NO VETTE DE L'AGRES DE L'AGRES DE L'AGRES PROFESSOR NO VETTE DE L'AGRES	AILKANLUNGE ASFVVFLIQER SYVSSTNLPVL	LVGRNLFA GGONDILE	LTGDTTVTRGDAFLNKNSILSNIHEVRÖNMGYCROFDATTBLITGREHVERFALLKGV PEKRYGKVGEMA, TRKLGLYKYGERYAGNYSGGNXRKLSTAMALIGGPPVYFLDEPTTG MDPRARRFLMNCALSYVKBGRSVVLTSHSMEBEDALCTRMAIMVNGRFRCLGSVQHLK MTANACOMMANATARGMANATARGMANATARGHEN	EGDGIIIVVKI ILSQSKKRLHI LQDEKVKESYV	2893. gene= numbe	"AB	79049 ="ABCAl" =r=5	/ulverioilo; /qene="ABGAl" /number=6 104155104328 /gene="ABGAl"

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NOTE: This record contains 73 individual
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14241: ____
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17072: conti
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                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research
                                                              IGGGGCCGGGACCCGCAGAGCCGAGCCGACCTTCTCTCCCGGGCTGCGGCAGGGCAGGG 240
                                                                                                  61 COGGCCGGGGAGGAGGAGCACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCA 120
                                                1 GGGCCCCCGCTCCACGTGCTTTCTGCTGAGTGAACTACATAAACAGAGGCCGGGAA 60
                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-Jan-2000) Whitehead institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 13, 2000 this sequence version replaced 91:6705871.
                                                                                                                                                     121 GCCCAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCCGTAATTGCGAGGGAGAGTGAG
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                                                                                                                                                                                                                                                                                                                                            AC021246 69570 bp DNA linear HTG 1
Homo sapiens clone RP11-1N1C, LOW-PASS SEQUENCE SAMPLING.
Length 201144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
------ project Information
Center project name: L2512
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 69576)
Birren,3., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome, clone RP11-1N10
Unpublished
 DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www-seq.wi.mit.edu
 Score 246.8; DB 9
Pred. No. 3.7e-57;
                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center clone name: 1_N_10
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AC021246.2 GI:9119882
 98.7%;
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                             Conservative
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                                                                                                                                                                                                                                                         241 CGGGGAGCIC 250
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    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  ETG:
                             Matches 248;
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AUTHORS
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arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                                                                                       will be sequenced to completion. In the event that the record is updated, the accession number will
sequencing reads that have not been assembled into
                   contigs. Runs of N are used to separate the reads and the order in which they appear is completely.
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880: gap of 100 bp

24733: contig of 853 bp in length
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: 851 bp in length
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contig of 878 bp in length
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if 800 bp in length
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gap of 100 hr
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76: gap of 1
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: gap of 10
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64783: contig of 856

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cont...
is of 1852 bp in control of 852 bp in 100 bp in length 4834 bp in length 484 bp in length
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contig of 863 bp in length
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contig of 840 bp in length
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55197: contig of 868 bp in length
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57163: contig of 866 bp in length
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44752: contig of 876 bp in length
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38083: contig of 855 bp in length
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32368: contig of 858 bp
68: gap of 100 bp
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Landerson. S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson. S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson. S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Choepel, Y., Colangelo, M., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Corlina, S., Collymore, A., Cooke, P., DeArellano, K., Dowino, M., Doyle, M., Fenestor, J., Farreira, P., Fitzingh, W., Forrest, C., Gade, D., Galagan, J., Gardyaa, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johason, R., Johes, C., Kan, L., Karatas, A., Klein, J., Macdonad, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Mopheters, R., Marquis, N., McEwan, P., McGurk, J., Norman, C.H., O'Contor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Peterson, R., Santos, R., Severy, P., Spencer, B., Stanger-Thoman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stanger-Thoman, D., Tirrell, A., Vassiliev, H., Viel, R., Wo, A., Wu, X., Myman, D., Ye, W. J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Myman, D., Ye, W. J., Direct Submission

Submitted (16-JaN-2005) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6705761.
All repeats were identified using RepeatMasker:
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                                                                                                                                                                                                Score 226; DB 2; Length 69570; Pred. No. 1.9e-51;
                64883; gap of 100 bp 65540; contig of 857 bp in length 65840; gap of 100 bp 66684; contig of 844 bp in length 65784; gap of 100 bp 67551; contig of 867 bp in length 67751; gap of 100 bp
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Homo sapiens, clone RP11-24J9
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28456: contig of 902
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                        ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                              * sequencing reads that have not been assembled into 
* contigs. Runs of N are used to separate the reads 
* and the order in which they appear is completely 
* arbitrary. Low-pass sequence sampling is useful for 
* identifying clones that may be gene-rich and allows 
* overlap relationships among clones to be deduced 
* However, it should not be assemmed that this clone 
* will be sequenced to completion. In the event that 
* the record is updated, the accession number will 
* be preserved.
     http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                 Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ project information
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[E. [ (Dases 1 to 697)]

Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aouizerat, B.E., Fielding, C.J. and Kane, J.P.

Analysis of hABC1 gene 5' end: acditional peptide sequence, promoter region, and four polymorphisms

L. Biochem. Blophys. Res. Commun. 271 (2000) In press

E. (bases 1 to 697)

E. (bases 1 to 697)

Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aouizerat, B.E., Fielding, C.J. and Kane, J.P.

Janet Submission

Submitted (19-APR-2000) Cardiovascular Research Institute, University of California, San Francisco, 505 Parnassus Avenue, San Francisco, CA 9413-0130, USA
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HOMO sapiens ATP binding cassette transporter 1 (ABCA1) mRNA, partial cds.
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                                                                                                                                                                                                                                                                 83.0%; Score 207.4; DB 2; Length 90698: 94.4%; Pred. No. 2.3e-46; Live 0; Mismatches 12; Indels 2;
                                                                                                                                              66955 67054: gap of 100 bp 67055 67947: contig of 893 bp in length 67948 68047: gap of 100 bp 68934: contig of 876 bp in length 68935 69334: gap of 100 bp 69035 69910: contig of 876 bp in length
                                                                                                                    oof 100 bp contig of 879 bp in length
                                                              100 bp
889 bp in length
                                                                                                        in length
                     in length
                                                in length
      tp of 100 bp
contig of 871 bp in 100 bp
contig of 904 bp in 100 bp
                                                                                        100 bp
f 860 bp
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                                                contig of
                                                                26: gap of 1
65015: contiq of
                                                                                                        contig of
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                           .122: gap of
.64026: crr.
                                                                                       115: gap of
65975: cont
                                                                                                                     gap of
                                                                                                                                                                                                                                       69911 70010: gap of
       62151: gap of
63022: cont
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                                   63123
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64027
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                                                                                                                                                                                                                                                                                                 Matches 236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
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JOURNAL
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AF258627
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KEYWORDS
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                                                                                                                                                             /product="ATP binding cassette transporter 1"
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198 0 156 1 100 g 156 t 1 thers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P., Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S. Regulatory nucleic acid sequences of the abci gene Patent: WO 0183746-A 3 08-NOV-2091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2735 GGGCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAACAGAGGCCGGGAA 2794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CEGGGCGGGGAGGAGGAGCACAGGCTITGACCGATAGTAACCTCTGCGCTCGGTGCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 AACTAGTCCCGGCAAAAACCCCGTAAIIGCGAGCGAGGGAGTGAGTGGGGCCGGGACCCGCA 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.0%; Score 157.4; DB 6; Length 2893; 99.4%; Pred. No. 1.3e-32; Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                          Length 697;
                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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8e-37;
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                                                                                                                                                                                                                                                                                                                                             11arity 100.0%; Pred. No. 8e-Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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AX351031
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1. .>697
                                                                                  396. .>697
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                                                                                                                                                    /codon_start=1
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Search completed: February 4, 2003, 01:37:29 Job time : 1021.76 secs

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ABL58400 standard;
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ABL58400
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8245.650 Million cell updates/sec
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2185239 seqs, 1125999159 residues
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                                                                                                                                                                                                       February 3, 2003, 12:46:48
                                                                                                                                         nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                CM nucleic
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		Human large ATP-bi	Nucleotide sequenc	Nucleotide sequenc	Euman ABC1 genomic	Human ABC1 transcr	Human ABC1 transcr	Human secreted pro	Human ATP binding	Human ATP binding
	ID		24 ABL58400	22 AAF24681	22 AAF24703	22 AAF92831	4 AAD37265	24 AAD37267	21 AAC09615	22 AAD21326	22 AAI70315
	h DB	1 1									
	Lengt	1 1 1 1 1 1	1297	1643	1643	183999	3231	2910	227	7260	7260
сφ	Query Match Length DB	111111	100.0	100.0	100.0	100.0	99.4	69.8	47.8	39.2	39.2
	Score		250	25C	250	250	248.4	174.4	119.4	86	90

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Result No.

	n cDNA clone	CDNA	clone	Hrman cDNA sedrenc	Human polynucleoti	Human ABCAl homolo	Human polynucleoti	Human ABC1 DNA seg	Nucleotide seguenc	ectide	Nucleotide sequenc	ectide	sotide	ectide s	Rat melanocortin r	ABC1 polymorphism		ncodin	Human cDNA 5'-end	CDNA	fuli-	clone	n extracellul	sot.	stomach can	cDNA sequen	aggred	ORFX ORF	oryza	protein HP	cancer age	in-5	rtin-5 r	anocort		
AAD3726	AAH0743	AAH1860	AAH0472	AAH1745	AAK5168	ABA0920	AAK5266	AAS0612	AAF24680	AAF2470	AAF2458	AAF2468	AAF2470	AAF2470	AAQ977(AAF9306	AAH9224	AAS8355	AAK921(AAK9354	AAK948.	AAH046	AAD080	AAH777	AAI938	AAH155	AAX007	AAC754	AAF140	AAF286	AAS608	AAT687	AAV623	AAV039	AAV064	
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ALIGNMENTS

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                                                                              transporter 1 (ACC1) promoter capable of directing transcription of heterologous coding sequence positioned downstream to it. The hABC1 promoter is useful for expressing foreign DNA in a host cell, by introducing into the host cell a gene transfer vector comprising the promoter operably linked to a foreign DNA encoding a desired polypeptide or RNA, where the foreign DNA is expressed. The gene transfer can be introduced into the host cell by adenovirus infection, liposome-mediated transfer, topical application to the cell or microinjection. The gene transfer vector encodes and expresses a reporter molecule. The method further involves introducing into the cell a gene transfer vector comprising a nucleic acid segment encoding a transactivator protein capable of upregulating the ABC1 promoter, or contacting the cell with the transactivator protein.

**Modulators of human ABC2 gene expression are useful for transactivator protein.**

**However the protein of the expression are useful for transactivator protein.**

**However the protein of the expression are useful for transactivator protein.**

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCGAAICTATAAAAGGAACTAGTCCCGGCAAAACCCCGTAAIIGCGAGCGAGTGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CGGGGGGGGGGGGGGGGGGGGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of the 5' flanking region of the human ABC1 gene.
                                                                   The invention relates to an isolated human large ATP-binding cassette
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGCCCCGGCTCCACGTGCTTTCTGCTGACTGACTGACTACATAAACAGAGGCCGGGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apolipoprotein-mediated mobilisation; cholesterol: Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                          atherosclerosis. The present sequence represents the hABC1 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             932 GGGCCCCGCCTCCACGTTCTCTGCTGACTGAACTACATAAAAAGAGGCCGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; adenosine triphosphate binding cassette protein 1; ABC1;
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e-66;
Matches 250; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                            Sequence 1197 BP; 284 A; 314 C; 328 G; 271 T; 0 other;
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                                       Claim 1; Fig 3; 68pp; English.
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99US-0153872.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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14-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF24681;
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The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (AIP) binding casette protein (ABC) I gene. ABCI resides in cell membranes and utilises ATP hydrolysis to transport a wide protein in the apolipoprotein mediated mobilisation of intracellular protein in the apolipoprotein mediated mobilisation of intracellular choiseterol stores. ABCI is defective in Tangier disease, a genetic disorder characterised by abnormal HBL-choiseterol metabolism. The ABCI gene is localised to chromosome 9q22-9q31. The ABCI genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGCCCGGCTCCACGTGCTTTCTGCTGACTGACTACATAAACAGAGGCCGGGAA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1643 BP; 370 A; 413 C; 457 G; 403 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 143-144; 215pp; English.
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                                                                                                                        Garvin M;
99US-0166573.
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                                                         (CVTH-) CV THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 250; Conservative
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                                                                                                                        Lawn RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (ATP) binding cassette protein (ABC) I gene. ABCI resides in cell membranes and utilises ATP hydrolysis to transport a wide protein in the apolipoprotein mediated mobilisation of intracellular pholesterol stores. ABCI is defective in Tangiar disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABCI gene is localised to chromosome 9422-9431. The ABCI genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosalenosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for screening assays with cholesterol transport. The genes and proteins are also useful for a screening assays with cholesterol transport. The genes and proteins are also useful for a screening assays with cholesterol transport. The genes and proteins are also useful for a screening and a screening 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCGTAATTGCCAGCGAGAGTGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CGGGGCGGGGAGGAGGAGGAGAGCACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGGGCCGGGACCCGCAGAGCCGAGCCTTCTCTCCCGGGCTGCGGCAGGGCAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1643 BP; 370 A; 413 C; 457 G; 403 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 138-139; 211pp; English
                                                                                                                                                                                                                                                                               Garvin M;
                                                                                                                                            99US-0140264.
99US-0153872.
99US-0166573.
                                                                                                                                                                                                                                                                           Oram JF,
                                                                                                                                                                                                                   (CVIH-) CV THERAPECTICS INC. (UNIW ) UNIV WASHINGTON.
                                                                                                             2000WO-US16591
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                                                                                                                                                                                                                                                                           Wade D,
                                                                                                                                                                                                                                                                                                                                                                                                          atherosclerosis
                                    WO200078971-A2.
                                                                                                           16-JUN-2000;
                                                                                                                                              18-JUN-1999;
                                                                                                                                                                 14-SEP-1999;
                                                                                                                                                                                 19-NCV-1999;
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Best Local Simi.
Matches 250;
                                                                         28-DEC-2000
                                                                                                                                                                                                                                                                         Lawn RM,
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The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-chokesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulares LXR- or RXX-mediated transcriptional activity or ABCI expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected a lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28751 GCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCGTAAITGCGAGCGAGAGTGAG 28810
                                                                                                      High density lipoprotein-cholesterol, HDL-C; cardiovascular; ABC1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGGGCGGGGAGGAGGAGGACACAGGCTTTGACCGATAGIAACCTCTGCGCTCGGTGCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 250; DB 22; 100.0%; Pred. No. 7.6e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pimstone SN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayden MR, Brooks-Wilson AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-2000; 2000US-0526193.
23-JUN-2000; 2000US-0213958.
                                                                                                                                                                                                                                                                                                                    01-SEP-2000; 2000WO-IB01492
                                                                                                                                                                                                                                                                                                                                                                                             2000US-0526193
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (XENO-) XENON GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                  Human ABC1 genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-244356/25.
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Best Local Similarity
Matches 250; Conservi
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                                                                                                                                                                                                             WO200115676-A2.
                                                                                                                                                              Homo sapiens
17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                    01-SEP-1999;
                                                                                                                                                                                                                                                                08-MAR-2001
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RESULT 5

AAF92831 standard; DNA; 183999 BP.

AAF92831 ID AAF9

Homo sapiens

08-NOV-2001

A NAME OF COLORS OF STREET OF STREET

21-AUG-2002

AAD37265;

AAD37265

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Human; AIP-binding cassette 1; ABC1 gene regulation; atherosclerosis; cholesterol metabolism; hypercholesterolaemia; antisense therapy; ds.
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/bound_moiety= "LMO2COM/MYOD/DeltaEF1"
549..556
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/bound_moiety= "HFH2/SRY/EVI1"
                                                                                                                                                                                                                                                                                                                                                                                 /bound_moiety= "LMO2COM/MYOD"
                                                                                                                                            Human ABC1 transcription regulatory DNA #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "CREBP1/VBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /bound_moiety= "S8/NKX2.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "DeltaEF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /bound_moiety= "DeltaEF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /bound_moiety= "NFY/CAAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "LKX2.5"
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.076..1089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /bound_moiety= "MZF1"
771..785
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/bound_moiety= "IX2"
412..420
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12..23
         BP.
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/bound_moiety=
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/bound_molety=
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528..539
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831..837
    AAD37267 standard; DNA; 2910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates a nucleic acid which is capable of regulating the transcription of human ATP-binding cassette 1 (ABC1) gene, which is a casual gene for patchologies linked to a dysfunctioning of cholesterol metabolism, including diseases such as atherosclerosis. Polynucleotides of the invention are used to screen candidate molecules or substances of that are capable of modulating the transcription of the ABC1 gene. They are used in antisense therapy. Compositions comprising sequences of the invention are used to treat hypercholesterolaemia and atherosclerosis. The present sequence is human ABC1 transcription regulating DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2735 GGGCCCGGCTCCACGTGCTTCTGCTGACTGAACTACATAAACAGAGGCGGGAA 2794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid useful for modifying the ATP-binding cassette l (ABCl) and screening for candidate modulatory compounds or substances \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CGGGGCGGGGAGGAGGAGGAAGGCTTTGACCGATASTAACCTCTGCGCTCGGTGCA 120
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ey A, Santamarina-Fojo
                                                                                                                                     Human ABC1 transcription regulatory DNA #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosier-Montus M, Prades C, Lemoine
Preus B. Duverger N, Remaley A,
    ВЪ
AAD37265 standard; DNA; 3231
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                                                                                         (first entry)
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CGGGGAGCTC 2984
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es 249; Conserv
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Query Match

Best Loca Matches

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protein_bind

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P-PSDB; AAE13022
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                    28-JAN-2002
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AAD21326;
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Matches
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                                                                                                                                                                                                                                                                                                                                                 The present sequence is one of a large number of 5' ESTS derived from manks according secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or poly4+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences to mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' URR is rarely included. 5' ESTs are derived from mRNAs with intect 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. expression and secretion vectors.
                                                                                                ; expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; ss.
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                                                                                                                                                                                                                                                                                                             diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
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1;
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                                                                             SEQ ID NO: 13690.
                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 13690; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                   Giordano
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0; Mismatches
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                                                                           Human secreted protein 5' EST,
                AAC09615 standard; cDNA; 227
                                                                                                                                                                                       21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                          99US-0122487
                                                         (first entry)
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1es 120; Conservative
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                                                                                               EST;
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                                                                                                         gene therapy;
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                                                                                                                                                EP1033401-AZ.
                                                                                                                                                                                                          26-FEB-1999;
                                                                                                                              Homo sapiens
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                                     AAC09615;
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                                                                                                                            Human; AT? binding cassette transporter 1; ABC1; coronary heart disease; defamatological; arberosclerosis; cardiovascular; inflammatory disease; psoriasis; lipid disorder; antibacterial; septic shock; gene therapy; immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to four common polymorphisms in the gene encoding APP-binding cassette transporter-1 (ABC1). ABC1 is associated with decreased AppA-1 mediated efflux of cholesterol. The polymorphisms in ABC1 directly affects cellular lipid homeostasis, which is a key factor diagnosing and treating lipid disorders, cardiovascular diseases (coronary heart disease, atherosclerosis) and inflammatory diseases (psoriasis, lupus erythematosus). The identification of ABC1 as a transporter for interleukin-lbeta (IL-lbeta) identifies this gene as a candidate for treatment of inflammatory diseases including rheumator architis and septic shock. The present sequence is human ABC1 gene.
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                                                                 Human ATP binding cassette transporter 1 (ABC1) gene.
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7.4e-20;
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321..7106
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(first entry)
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es 98; Conserv
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The present sequence is that of cDNA encoding the human adenosine triphosphare (ATP) binding cassette transporter I (ABCI) protein (see AAM5022). The sequence includes an extended open reading frame (ORF) to that provided by the sequence in AA70314, using an alternative ATG codon as initiation codon and thereby adding an extra 40 N-terminal main:0 acids to the encoded ABCI protein (see AAM5028). The invention provides 4 common polymorphisms in the ABCI gene. These were identified by sequencing the ABCI gene in ABCI gene. These were identified by sequencing the ABCI gene in ABCI gene. The changed to A at position 596, T is changed to C at position 135, A is changed to G at position 2589 or G is changed to C at position 135, A is changed to G at position 2580 or G is changed to C at position 135, A is changed to G at position 2580 or G is changed to C at position 2580, T is changed to G at position 2580 or G is changed to C at position 2580, T is changed to Mark a decreased in vitro ApoA-I madiated efflux of cholesteroi from monourclear phagocytes, a relative typical of Tangier Gisease. 3 Of the variants (G556A) and A2589G and G3456C) are significantly increased in a population of methatic physical or methated efflux this and therefore and A2589G and G3456C) are significantly increased in a population of methatic physical or propertien cholesterol included the content of the variants (G596A) are higher cholesterol included the content of the variants (G596A) are higher cholesterol included the content of the variants (G596A) are higher cholesterol included the cholesterol
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/note= "alternative open reading frame of AAI70314"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New adenosine triphosphate binding cassette transporter gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                             ATP binding cassette transporter 1; ABC1; human; lipid disorder; colossersol; cardiovascular disease; inflammatory disease; antiinflammatory; antilipic; antiipscriatic; dermatological; Tangler disease; coronary heart disease; diagnosis; gene therapy;
Human ATP binding cassette transporter 1 (ABC1) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 26-28; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= &
replace(2969,G)
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/*tag= f
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/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAR-2000; 2000EP-0106401
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/*tag= a
7106
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                                                                                                                                                                                                                                                                                                       polymorphism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAM50228
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates a nucleic acid which is capable of regulating the transcription of human ATP-binding cassette 1 (ABC1) gene, which is a casual gene for pathologytes linked to a dysfunctioning of cholesterol metabolism, including diseases such as atherosclerosis. Polynucleotides of the invention are used to screen candidate molecules or substances that are capable of modulating the transcription of the ABC1 gene. They are used to treat hypercholesterolaemia and atherosclerosis. The present sequence is human ABC1 gene exon 1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modifying the ATP-binding cassette 1 te modulatory compounds or substances
                                                                                          153 AAACCCCGTAATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCCACCC 212
                                                                                                                                                                                                                                                                                                                                                                                      Human, ATP-binding cassette 1, ABC1 gene regulation, atherosclerosis,
cholesterol metabolism, hypercholesterolaemia; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 GTAATTGCGAGCGAGAGTGAGTGGGGCCCGGAACCCGCAGAGCCGAGCCGAACCCTTCTCTC 219
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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Duverger N, Remaley A, Santamarina-Fojo S;
                              Length 7260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 221;
Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
                                DB 22; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 221 BP; 44 A; 62 C; 73 G; 42 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.4%; Score 91; DB 24; 1
100.0%; Pred. No. 3.6e-18;
                                                                                                                                                     213 ITCTCTCCCGGGCTGCGGCAGGCCAGGCCGGGGAGCTC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABC1) and screening for candidate modulatory
                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismacches
                              39.2%; Score 98; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 132; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            larity 100.0%; P
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAY-2001; 2001WO-EP05488
                                                                                                                                                                                                                                                              AAD37268 standard; DNA; 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAY-2000; 2000US-201280P
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                       Human ABC1 gene exon 1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AVET ) AVENTIS PHARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2032-154404/20.
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es 91; Conserv
                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200183746-A2.
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                                                           .86
                                                                                                                                                                                                                                                                                             AAD37268;
                                Query Match
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                                                           Matches
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the specification. The primer sets can be used in antisense tnerapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length conas. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length conast of the abnormality of the full-length conast allow obtaining of the full-length conast and antibout any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18642 represent human conast sequences; AAB92446 to AAH13632 AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhe present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs ^{-}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saito K, Ya
, Otsuki T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID 4267; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA clone (5'-primer) SEQ ID NC:4267.
220 CCGGGCTGCGGCAGGCAGGCGGGGGGGGAGCTC 250
                                    61 CCGGGCTGCGCCAGGGCAGGGCGGGGAGCTC 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                        AAH07432 standard; cDNA; 736
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                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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The present invention describes primer sets for synthesising 5602 comprises: (a) an oligo-dT primer and an oligonucleotide complementary strand of a polynucleotide which complementary trand of a polynucleotide which comprises one of oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence complementary to a polynucleotide comprises at 1-east 15 nucleotides and the combination of the 5'-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                                                                                                   Human; primer; detection; dlagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the full-length cDNas. The primers allow obtaining of the full-length cDNas easily witcout any specialised methods. AAH03165 to AAH13528 and AAH13633 to AAH13642 represent human cDNa sequences; AAB92446 to AAH13639 represent human and sequences; and AAH13629 to AAH13632 represent oligocucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
 219
Yamamoto J; T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito K,
Otsuki
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A, Nagai F
                                                                                                           92
                                                                                          220 CCGGGCTGCGGCAGGGCAGGCGGGGGAGCTC
                                                                                                                                                                                                                                                                                                                Human cDNA sequence SEQ ID NO:18808,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                   AAH18506 standard; cDNA; 1555
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20007P-0118776.
20007P-0183767.
20007P-0241899.
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                                                                                                                                                                                                                                                                            (first entry)
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27-AUG-1999;
11-JAN-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oliqor-dT primer and an oliqornucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence complementary to a polynucleotide onprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                             primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                           160 GTAATTGCGAGGGGAGAGTGGGGGCGGGACCCGCAGGCGGAGCCGACCCTTCTCTC 219
                                                  Gaps
                                                                                          Yamamoto J;
                                                  .;
o
                          Length 1556;
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                                                    Indels
BP; 380 A; 363 C; 399 G; 414 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito K,
                       35.8%; Score 89.4; DB 22; 98.9%; Pred. No. 2e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagai K,
                                     Pred. No. 2e-17;
0; Mismatches
                                                                                                                                                                                                                                                                                                     Human cDNA clone (5'-primer) SEQ 1D NO:1564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashi K,
                                                                                                                               CCGGGCTGCGGCAGGCCGGGGGGGCTC 250
                                                                                                                                              61 CCSGGCTGCGGCAGGGCGGGGGGGCTC 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nishikawa T,
                                                                                                                                                                                                                        ВР.
                                                                                                                                                                                                                       AAH04729 standard; cDNA; 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-1999; 995P-0300253.
11-JAN-2000; 2600JP-0118776.
02-MAY-2000; 2000JP-6183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-3248036.
                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-2000; 2000EP-0116126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000JP-0241899
                                                                                                                                                                                                                                                                           (first entry)
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-318749/34.
                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       full-length cDNAs
 Sequence 1556
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                           Query Match
                                                                                                                                                                                                                                                 AAH04729
                                                                                                                               220
                                                    Matches
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                                                                                                                                                                                              RESULT 13
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises. (a) an olico-di primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the polynucleotide which comprises a 3'-end sequence, where the polynucleotide comprises a 3'-end sequence, where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH35893 represent human amino acid sequences, and AAH13629 to AAH13632 represent oligonuclectides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                           1 AATTGCGAGCGAGCGAGTGGGGCCGGGACCCGCAGCCCAGCCCAGCCCATCTCCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto J;
                                                                                                                                                                                                              Length 763;
                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saito K,
Otsuki
                                                                                                                                                   Sequence 763 BP; 137 A; 205 C; 260 G; 158 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; SEQ ID 16905; 2537pp + CD ROM; English.
                                                                                                                                                                                                        Score 89; DB 22;
Pred. No. 2.1e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nishikawa T, Hayashi K, S
T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                              100.0%; Pred. No. -
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGCTGCGGCAGGCCAGGCGGGGGGGCTC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCTGCGGCAGGGCAGGCGGGGAGCTC
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11-JAN-2000; 2000JP-0118775.
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                                                                                                                                                                                                           35.6%;
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                                                                                                                                                                                                                                                                    89; Conservative
                                                                                             of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sugiyama
                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1074617-A2
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Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH17451;
                                                                                                                                                                                                              Query Match
Best Local 3
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AAH17451
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in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length AAH13633 to AAH13631 to AAH13632 represent human cDNA sequences; AAH23646 to AAH13632 represent human amino acid sequences; and AAH13632 to AAH13632 represent coligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy;
vaccine; peptide therapy; stem cell growth factor; haematopolesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                162 AATTGCGAGCGAGAGTGAGTGGGCCGGGACCGCAGAGCCGAGCCGAGCCTTCTCTCCC 221
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ма
                                                                                                                                                                                                                                                Nucleic acids encoding polypeptides with cytokine-like activities, useful is diagnosis and gene therapy -
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Wang 2
                                                                                                                                                                        Score 89; DB 22; Length 1750;
                                                                                                                                                                                                    C; Indels
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                                                                                                                                            Sequence 1750 BP; 291 A; 489 C; 586 G; 384 T; 0 other;
                                                                                                                                                                                       2.7e-17;
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ang J, Ren F, C
                                                                                                                                                                                    100.0%; Fred. No. 2.7
live 0; Mismatches
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Wejhrman T, Goodrich R;
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                                                                                                                                                                                                                                                                                         GGGCTGCGGCAGGGCAGGCGCGGGAGCTC 250
                                                                                                                                                                                                                                                                                                          61 SGGCTGCGGCAGGGCAGGGGGGGGGGGCTC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polynucieotide SEQ ID NO 228.
                                                                                                                                                                                                                                                                                                                                                                                          AAK51683 standard; cDNA; 7281 BP
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Wang J, Zha
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2000US-0560875,
2000US-0598675.
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20000S-0693325.
20000S-0728422.
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2000US-0654936.
                                                                                                                                                                         35.6%;
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Matches 89; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAM78550
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20-JUN-2000;
19-JUL-2000;
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15-SEP-2000;
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30-NOV-2000;
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cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopolosis requiating activity, issue growth factor activity, immunomodulatory activity and activity insue constructions.
                                                                                                                                                                            Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                              153 AAACCCCGTAATTGCGAGCGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCC 212
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      treatment of cancer, leukaemia, nervous system disorders, arthritis inflammation.
                                                                                                                                                                                                                                                                                                              Length 7281;
                                                                                                                                                                                                                                                                     Sequence 7281 BP; 1831 A; 1773 C; 1915 G; 1762 T; 0 other;
                                                                                                                                                                                                                                                                                                            30.9%; Score 77.2; DB 22;
86.7%; Pred. No. 1.7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 TTCTCTCCCGGGCTGCGGCAGGCCAGGGCGGGGGGGCTC 250
                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Database

Result No.

Sequence:

Gallus ga Drosophil Drosophil Drosophil

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AL072357 Drosophil
AL072367 Drosophil
AL0736825 Acrosophil
BQ73485 ACRNCOURT
AL05652 Drosophil
BP313090 601896494
BF213090 601896494
BF213090 601896494
BF213090 601896494
BF7541 BB17541 BB17541
BM769269 UT-M-FIO-
AL108460 Drosophil
BM810185 ACRNCOURT
AL47552 T brucei
BM810185 ACRNCOURT
AL47552 T brucei
BM810185 602528705
BG201366 602547706
BE809325 601517210
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BE809325 601517210
BE173210 Tetraodon
BE173210 Tetraodon
BC75018 602650162
BM5898865 ACRNCOURT
BM5889865 ACRNCOURT
BM588602 ACRNCOURT
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BM912186 AGENCOURT
BM912207 AGENCOURT
AG132188 Pan trog1
B1994587 103101390
BES94587 1031078F1
BE726743 894093C09
                                                                                                                                                                                                                                                                                                                                                         AJ135588 PLACE1 Homo sapiens cDNA clone PLACE1002437 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 736) Ota; T., Nishikawa; T., Sizuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 smail: genomics@hri.co.jp HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and
ALC65775 |
AJ231825 |
ALL06545 |
ALL01653 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRI human cDNA project
Unpublished (2000)
Contact: Takaor Isogai
Conmics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
        GGA200110
CNS016BR
                                                                                                                                        TA376C03P
BM762473
                              CNS00GP3
CNS0091P
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CNS0052P
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BF274287
BM915366
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BG501356
BI890368
BE889325
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BM912186
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BQ769269
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BM810185
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BM559867
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BM912602
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782
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1432
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sequence.
AUI35588
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LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                           RESULT 1
AU135588
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AU121731 AU121731
Z44377 HSCILSB081 n
BC034624 HOMO Sapi
BG678861 602624760
                                                 ; Search time 473.043 Seconds (without alignments) 8559.210 Million cell updates/sec
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      GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                   hits satisfying chosen parameters:
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2 AATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTICTCTCCC 61
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DXF2D686N12109_c1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DXF2G68N12109 5', mRNA sequence.
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Mammalia, Eutherla, Primates; Catarrhini; Hominidae, Homo.
1 (Jases 1 to 547)
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemenn, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email S.wiemann@dkfz- heidelberg.de;
sequenced by Qiaqen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No sI sequence available.
This clone (DKRZp686N12109) is available at the RZPD in Berlin. Please contact the RZPD Ressourcenzentrum, Heubnerweg 5, 14059 Berlin-Charlottenburg, GERMANY: Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                                                                                                                                                                                                                                                 160 GTAATTGCGAGGGGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCGGACCCTTCTCTC 219
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/db_xref="taxon:9606"
/clone="bkFzp686N12109"
/clone="bkFzp686N12109"
/clone="tb="686 (synonym: hicc3)"
/tissue_type="human skeletal muscle"
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                                                                                                                                                                                   Score 89.4; DB 9;
Pred. No. 5.1e-15;
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                                                                                                 /tissue_type="placenta"
/note="Vector: pME18SFL3"
199 c 199 g 170
                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1002437"
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Location/Qualifiers
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                                                                                /clone_lib="PLACE1"
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/lab_host="DH10B"
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EST (Duesterhoeft, et al.)
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Contact: Duesterhoeft A
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162 AATIGCGAGCGAGAGTGAGTGGGGCCGGGACCCGAGAGCCGAGCCGACCCTTCTCTCCC 221

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AU121731 NAMMAL Homo sapiens cONA clone MANMA1000851 5', mRNA sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 292)
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Mammalia: Butheria: Primates; Catarrhib; Hominidae; Homo.
I (bases 1 to 763)
Ota/T., Nishikawa/T., Suzuki/Y., Isrii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genomics@hri.co.jp
HRI human cDNa project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNa library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="mammary gland"
/note="Vector: pME18SFL3"
205 c 260 g 158 t
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/db_xref="taxon:9606"
222 GGGCTGCGGCAGGGCAGGCGGGGAGCTC 250
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                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 81-438-52-3986
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Matches 89; Conserva
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/dev_stage="3 months old.
/dev_stage="3 months old.
/dev_stage="3 months old.
/ince="lorgan: brain, Vector: lafmid BA; Site_1: MindIII;
/ince="lorgan: brain, Vector: lafmid BA; Site_1: MindIII;
/ince="lorgan: brain of the language of the cotal brain of the language of the language of the lafmid BA vector. Clone library from B.Soares, Psychiatry Bento Soares, P.N.A.S in press.

87 columbia University, USA. Normalization_method:
87 columbia Diversity, Soares, Soares, Soares, Bento Soares, Boares, Boare
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Auffray, C., Betar, G., Bois, F., Bouchier, C., da Silva, C., Devignes M.D., Duprat, S., Houlyate, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage Samson, R., Pietu, G., Pouliot, Y., Sebastiani - Kabaktchis, C. and Tessier, A.
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Submitted (24-010-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                               IMAGE: molecular integration of the analysis of the human genome
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Genexpress_library_idt: C; Genexpress_sequence_idt: ylc-lzb08
Seq primer: (-21)Ml3_universal.

Location/Qualiflers
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1,rue de 1'Internationale, BP60 91002 EVRY Cedex, FRANCE
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100.0%; Pred. No. 5.2e-11;
.ive 0; Mismatches 0; Indels
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: James Cleaver, M.D.
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/db_xref="taxon:9606"
/clone="c-1zb08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genexpress@genethon.fr
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                                                                                                                                                                                                                                                                                                                                                                                          Tel: 33169472800
Fax: 33160778698
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BG678861 602624760F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4749735 5', mRNA sequence.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5915657 This clone is the following problem: incomplete processing:
                                                                                                                                                                                           Contact: amg@bcm.tmc.edu
dardia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIE-MGC http://mgc.aci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="9kin, squamous cell carcinoma"
/clone_lib="NCI_CGAP_5kn4"
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Plate: LLAM10603 row: 9 column: 16
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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ilarity 100.0%; Pred. No. 6.7e-11;
Conservative 0; Mismatches 0;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
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/db_xref="taxon:9605"
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- Web: www.genoscope.cns.fr

- Setzermination of this 3AC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster aAC library was prepared by Kazutoyo Googawa and Aaron Mammoser in Pieter de Jong's Laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual 3AC clones, the entire library, or filters for hybridization from the 3ACPAC sescure Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              512 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR14804 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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/clone="LaAGE:4749735"
/clone=lib=NCL_CGAP_Skn4"
/tlssue_Ltype="squamous cell carcinoma"
/lab_host="NHDE (TI phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI:
/note="Organ: skin; NotI: Site_1 (Site_1 (Si
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Ephydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                                                                                                                                                                                                                   Length 998;
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/db_xref="taxon:7227"
/clone="BACR14H04"
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                                                                                                                                                                                                                                                                                                                                                      24.1%; Score 60.2; DB 12; 89.0%; Pred. No. 1.1e-06; varive 0; Mismatches 8;
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/note="end : TET3"
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Smith,J., Bruley,C.K., Paton,I.R., Dunn,I., Jones,C.T., Windsor,L
Morrice,D.R., Law,A.S., Masabanda,J., Sazanov,A., Waddington,D.,
Fries,R. and Burt,D.W.
Differences in gene density on chicken macrochromosomes and
microchromosomes
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                                                                                                                                                              Madauly Lower, Page 1998) Division of Molecular Biology, Roslin Submitted (12-AUG-1998) Division of Molecular Biology, Roslin Institute, Roslin, Midlothian ER25 9PS, Scotland, UK
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                                                                                         634 VVGMGVGMGAGGRGVGMGMMMMRRRGVAMGVGMGSSMCCSCMCMCGSGVGRGGSGVGSGC
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Archosauria, Aves: Necgnathae, Galliformes, Phasianidae;
Phasianinae, Gallus.
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/db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                 Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk · .This Drosophila melanogaster BAC library (Uros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS 25-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                              d'Etudé du Polymorphisme Humain) with funding proviced by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                               Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
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Drosophila melanogaster genome survey sequence T7 end of BAC BACN15K14 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                  Eukaryota; Metazoa, Artiropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /crganism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN15K14"
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16.0%; Pred. No. 3.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /plasmid="pBeloBACil"
/note="end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="DrosBAC"
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                                                                                                                 Drosophila melanogaster.
                                                                                                                                  Drosophila melanogaster
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                                                                       AL106545.1 GI:5622456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        pBeloBAC11
                                                                                                                                                                                                                              Genoscope
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                                                                                               GSS.
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   DEFINITION
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CNS012JV
                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
JOURNAL
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Drosophila melanogaster genome survey sequence T7 end of BAC: BACR$B116 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic envisor management (fruit fly), genomic envisor monthly and prosophila melanogaster (fruit fly), genomic envisor monthly and prosophila melanogaster (fruit fly), genomic envisor monthly and prosophila melanogaster (fruit fly).
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                                                                                                                                                                                                                        When www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (BDGP) - http://www.edgp.ebi.ac.uk. - This Drosophila me.anogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre of Etude du Polymorphisme Humain) with funding provided by a MRC and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                          Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequescage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref§genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   956 CRGSAACACASACMMCACSACACAAAMSAMGRMCCVASARSACARACASGAGCAMACAGMG 1015
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Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDGP The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 TAGTAACCTCGGCTCGGTGCCAGCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACC 157
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Drosophila melanogaster
Eukaryota; Metazca; Arthropoda; Hexapoda; Insecta; Pterygota;
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Length 1101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 others
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/organism="Drosophila meianogaster"
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1 (bases 1 to 1101)
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34.0%; Pred. No. 4.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /close_lib="DrosBAC"
/plasmid="pBeloBAC11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 ICCCGGGCTGCGGCAGGGCGG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="BACN08M13"
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Best Local Similarity 34.09
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source

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Web: Www.genoscope.cos.fr.

Web: Www.genoscope.cos.fr.

Web: Www.genoscope.cos.fr.

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drsophila denome Project (BDGP).

The BGGP is constructing a physical map of the Drosophila melanogaster genome using these 3Acs. For further information please see http://www.fruitfly.org The BGGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The Library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2: cn bw sp, the same strain used for the BDGP's pland mass or an analysis and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.mad.buffalo.edu/drosophila_bac.htm.
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melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be iccation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      861 AMMCKAGCGGGGGGGGGRARRAGRGGGGGRAGCSRAGMGGMGAACDSCKKKKCAARNAD 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 CTGCGCTCGGTGCCAGCCGAATCTATAAAGGAACTAGTCCCGGCAAAAACCCCGGTAATTG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 921 KAKAKDKANKADCRKKMKAAKMAGARCAMASARAGAAAAGSGMGAAVCGCACAGCAAAAR $80
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/db xref="taxon:7227"
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41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="BACR33E16"
/clone_lib="RPCI-98"
/cote="end : 17"
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es 53; Conservative
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Matches
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS 26-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN16D22 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL106855
AL106855.1 GI:5624152
                                                                                                                                                                                                                                                                                                                                                                                                                                               661 SCSSSSMSASSSSASSSSSSSSSSSSSSACGBSMSSGGGSGSVSASSGMSSSVSSS 602
                                                                                                                                                                                                                                                                                                                         107 CIGCGCICGGIGCAGCCGAAICTAIAAAGGAACTAGICCCGGCAAAAACCCCGGTAAIIG 165
                                                                                                                                                                                                                                          47 ACAGAGGCCGGGAACGGGGGGGGGGGGGGGGGGGCACAGGCTTTGACCGATAGTAACCT 106
                                                                                                                                                                                                                                                                          Gaps
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1 (bases 1 to 1100)
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                                                                                                   511 others
  melanogaster"
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/db_xref="taxon:7227"
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                                                                                                                                                                                                    95; Mismatches
                                                                                                                                                                                 Pred. No. 12;
                                                                                                                                                            14.2%; Score 35.4;
13.6%; Pred. No. 12
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22.4%; Pred. No.
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/organism="Drosophila
/db_xref="taxon:7227"
/clone="3ACR19D16"
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                                                         /clone_lib="RPCI-98"
/note="end : TET3"
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229 c 106
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BASE COUNT
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//ab_lost="Organ: Spleen; Vector: pOTB7; Site_1: XhoI: Site_2:
ECGRI; CDNA made by Oligo-dr priming. Directionally cloned
into EccRIXXhol sites using the following 5 adaptor:
GGCACCAG(G). Library constructed by Ling Hong in the
laboratory of Geraid M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Strategene) and
Superscript II RT (Life Technologies). Note: this is a
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                                                                                                                                                                                                                                                                                                                                                    967 bp mRNA linear EST 16-JUL-2302
1.113 Homo sapiens cDNA clone IMAGE:6301501
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Euxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 967)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                          913 VVGMGMGMGMGWGWVMCGMGWVVMGMRRAGGVGMMGMRAGMGGMMRMAVMRHMMMHG 854
                                                                                                                                               148 GGCAAAAACCCCGTAATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGGCC
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                                  973 GVGVGRMRVKMVMGEMGMRNGKGVGGVMGGGMRGKVGGGVVMGVGCMGMGVGKVGKVGMVGM 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
found through the E.M.A.G.E. Consortium/Library
Arrayed by: Agencourt Bloscience Corporation
found through the E.M.A.G.E. Consortium/LINL at:
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Pred. No. 17
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/clone="IMAGE:6301601"
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5', mRNA sequence.
BQ708275
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48.9%;
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nes 87; Conserv
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/Organis...
/db_xref="taxon:90uv"
/clone="IMAGE:6254865"
/clone="IMAGE:6254865"
/clone="IMAGE:6254865"
/clone="IMAGE:6254865"
/clone="IMAGE:6254865"
/tissue_type="epidermoid carcinoma, cell line"
/tab_host="Dalba (piage-resistent)"
/note="Organ: salivary gland: Vector: poTB7; Site_1: XhoI;
Site_2: EcoRI; cDN made by oligo-dr priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAGG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
"echnologies). Note: this is a NIH MGC Library."
/stl q 69 t 39 others
                                                                                                                                                        BQ673465 119C bp mRNA linear EST 15-JUL-2002 AGENCCURT_8189102 NIH_MGC_1C2 Homo sapiens cDNA clone IMAGE:6254865
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CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.W.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.W.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
High quality sequence stop: 226.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D. Email: cgapbs.r@mil.nih.gov
Tissue Procurement: ATCC
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Best Local Similarity
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Search completed: February 4, 2003, 03:27:02 Job time : 487.757 secs

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FILING DATE:
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CLONE: pIZgpt-Fls
US-08-232-463-14
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GENERAL INFORMATION:
USA
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6534.066 Million cell updates/sec
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                                                                                                                                                                                                                    2003, 12:56:40 ; Search time 11.7338 Seconds
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seg:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seg:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seg:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seg:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seg:*
                       GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-446-872A-68
US-08-446-872A-70
US-08-746-72A-71
US-08-762-227A-71
US-08-762-227A-71
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PCT-US95-01185-68
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US-09-222-126B-14
US-08-672-126B-9
US-08-672-109B-9
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US-08-84-2045-9
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US-08-629-335B-9
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US-08-469-318-71
US-08-468-609A-68
US-C8-468-609A-70
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US-08-459-318-68
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length
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Seguence 5,
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                   APPLICANT: BORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                            US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AGG-1991
ATTORNAY/AGENT INFORMATION:
NAMB: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
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APPLICATION NUMBER: US/07/935,313
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Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 2233-029
COMPUTER READABLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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(703)683-4109
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SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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                                                   Length 3250;
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PAPLICANT: Gantz, Ira
TITLE OF INVENTION: Genes Encoding Melanccortin Receptors
NUMBER OF SEQUENCES: 23
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Satent No. 6451575
SEMERAL INFORMATION
TILLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES
FILE REPERENCE: DM6909
CURRENT APPLICATION NUMBER: US/09/122,1268
CURRENT APPLICATION NUMBER: US/09/122,1268
NUMBER OF SEQ ID NOS: 21
SGOTWARE: Patentin version 3.0
LENGTH: 3250
                 83;
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63.3%; Pred. No. 0.82;
tive 0; Mismatches 29;
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Best Local Similarity 8.0%; Pred. No. 0.2; Matches 17; Conservative 113; Mismatches
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Patent No. 5703220
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Best Local Similarity vo...
Than 50; Conservative
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CITY: Bloomfield Hills
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (121)..(2910)
US-09-122-126B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-09-122-126B-14/c
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NAME/KEY: CDS
LOCATION: (121
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89 ITTGACCGALAGTAACCTCTGCGCTGCAGCCGAATCTATAAAAGGAACTAGTCCCG 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.5%; Score 31.2; DB 1; Leigth 975; 47.1%; Pred. No. 1.5; tive 0; Mismatches 108; Indels
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VS.08-672-109B-9/c

/Sequence 9, Application US/08672109B

/ Patent No. 5710265

/ GENERAL INFORMATION:

/ APPLICANT: Yanda, Tadataka

/ APPLICANT: Cantz, Ira

APPLICANT: Gantz, Ira

APPLICANT: Genes Encoding Melanocortin Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATIVE SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/572.109R
                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deadn F.
REGISTRAHION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 2115-000853DVB
TELECOMMUNICATION INFORMATION:
                                                             US/08/671,525B
PC-DOS/MS-DOS
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                                                       APPLICATION NUMBER: US/08//
FILING DATE: June 27, 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                             (810)641-1600
                                                                                                                                                                                                                                         TELEFAX: (810)641-0270
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                       : 975 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 47.15
Matches 96; Conservative
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MEDIUM TYPE: Floppy
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STREET: P.O. Box 826
  OPERALING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                       linear
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HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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LOCATION:
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COUNTRY:
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89 TITGACCGATAGTAACCTCTGCGCTCGCTGCAGCCGAATCTATAAAAGGAACTAGTCCCG 148
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APPLICANT: Gantz, Ira
TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
NUMBER OF SEQUENCE: 23
CORRESPONDENCE ADRESS:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC_COMPatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Mismatches 108;
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                   2115-000853DVE
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              REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPANE: (810)641-1600
TELEFAX: (810)541-0270
REGISTRATION NUMBER: 36683
                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                   : 975 base pairs
nucleic acid
                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96; Conservative
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                                                                                                                                                                              double
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                                                                                                                                                                                                                                                                                                         Mouse
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                                                                                                                                                             TYPE:
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: Genes Encoding Melanocortin Receptors
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.5%; Score 31.2; DB 1;
47.1%; Pred. No. 1.5;
tive 0; Mismatches 108;
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                                                                                         REFERENCE/JOCKET NUMBER: 2115-000853DVC TELECOMMUNICATION INFORMATION: TELEPHONE: (810)641-160C TELEFAX: (810)641-0270 INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08842045
Patent No. 5817787
GENERAL INFORMATION:
APPLICANT: Yamada, Tadataka
APPLICANT: Genes, Ira
TITLE OF INVENTION:
UMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 ACCCTTCTCTCCGGGCTGCGGCA 232
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June 27, 1996
                                                                        REGISTRATION NUMBER: 36683
                                                                                                                                                                                                                                                                                                       DNA (genomic)
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NAME: Smith, DeAnn F.
                               ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
                                                                                                                                                                                                                    LENGTH: 975 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Harness, Dic
STREET: P.O. Box 828
CIIY: Bloomfield Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 96; Conserva
                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                1..975
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mouse
                   CLASSIFICATION:
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HYPOTHETICAL: N
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US-08-842-045-9/c
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STATE:
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TITLE OF INVENTION: Methods and Reagents for Discovering and TITLE OF INVENTION: Using Mammalian Melanocortin Receptor Agonists and Antagoni TITLE OF INVENTION: To Modulate Feeding Behavior in Animals
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                                                                                                                                                                                                                                                                                                                                                                                                      89 ITTGACCGATAGTAACCTCTGGGCTGCAGCCGAATCTATAAAAGGAACTAGTCCCG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                          551 TTGGACTCATAGTAGATGATGAAAACAATGCCGCAGCTTATGCAGAAGGTCCAGATGCAG 492
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                                                                                                                                                                                                                                                                                                                            :0
                                                                                                                                                                                                                                                  Length 975;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DAIA:
                                                                                                                                                                                                                                                  12.5%; Score 31.2; DB 3;
47.1%; Pred. No. 1.5;
Live 0; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JMBER: US/08/706,281A
04-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: No. 6100048nan, Kevin 3
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886
IELECOMMUNICATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/08706281A Patent No. 6100048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 ACCCTTCTCTCCGGGCTGCGGCA 232
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Fan, Wei
Boston, Bruce A
Kesterton, Robert A
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IBM PC compatible
                                           DNA (genomic)
NO
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Chen, Wenbiao
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 47.19
Matches 96; Conservative
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TELEFAX: 312-913-0002
TELEX:
     TYPE: nucleic acid
STRANDEDNESS: double
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                                 MOLECULE TYPE: DNA (
HYPOTHETICAL: NO
ANTI-SPACE
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                                                                                                                                                                                             1..975
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                                                                                                                                     ORGANISM: Mouse
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                                                                                               ANTI-SENSE: NO ORIGINAL SOURCE:
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US-08-706-28LA-17/c
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US-08-629-335B-9
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APPLICANT:
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APPLICAN: Yamada, Tadataka
APPLICAN: Gantz, Ira
TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                        Score 31.2; DB 2; Length 9 Pred. No. 1.5; 0; Mismatches 108; Indels
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CURRENT APPLICATION DARS:
APPLICATION NUMBER: US/08/629,335B
FILING DATE: July 23, 1996
CLASSIFICATION: 435
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STREET: P.O. Box 828
CITY: Bloomfield Hills
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 9, Application US/08629335B
; Patent No. 6117975
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FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deang?
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TELECOMMUNICATION INFORMATION:
                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                        12.5%;
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TELEFAX: (810)641-0270
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 975 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                             ORGANISM: Mouse
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                                                                                                                                                                                                                                              ) NAME/KEY;
; LOCATION;
US-08-842-238-9
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ORIGINAL SO
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STATE:
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Sequence 68, Application US/08469318 Patent No. 6022535 GENERAL INFORMATION:
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   MOLECULE TYPE: DNA (genomic)
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MOLECULE TYPE: DNA (genomic)
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                                                      LOCATION: 1..975
SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACIERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                    NAME/KEY: CDS
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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Best Local Similarity
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                     FEATURE
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                                                                                                                                                                                                                                         Gaps
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TITLE OF INVENTION: Mammalian Melanocortin Receptor and Uses
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                       0;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AITORNEY/AGENT INFORMATION:
NAME: NO. 677803805n, Revin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886-C
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FILING DAIE: 12-Jum-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCCITCTCTCCCGGGCTGCGGCA 232
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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COMPUTER READABLE FORM:
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Best Local Similarity 47.1%
Matches 96; Conservative
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                                 978 base pairs
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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STATE: Illinois
                                               TYPE: nucleic acid
STRANDEDNESS: single
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US-08-706-281A-17
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                                                                                                                                       Gaps
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                                                                          Query Match 12.5%; Score 31.2; DB 4; Length 978; Best Local Similarity 47.1%; Pred. No. 1.5; Matches 96; Conservative 0; Mismatches 108; Indels
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SEQ ID NO: 17:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                           Multivariant IS-3 Rematopolesis Fusion Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 966;
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                                                                                                                                                                                                                  OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 30; DB 3;
Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-08-469-318-71/c;
; Sequence 71, Application US/08469318
; Patent No. 6025335
ceneral INFORMATION:
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/446,872
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                  Sequence 70, Application US/08469318 Patent No. 6022535 GENERAL INFORMATION:
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IBM PC compatible
                                                                                                                                                                              3: Floppy disk
IBM PC compatible
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MOLECULE TYPE: DNA (genomic)
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196
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                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                          966 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 49.45
Matches 78; Conservative
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INFORMATION FOR SEQ ID NO:
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LENGTH: 966 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           IYPE: nucleic acid
STRANDEDNESS: gouble
                                                                                                                                       NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
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                                                                                                 TITLE OF INVENTION:
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CLASSIFICATION:
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COMPUTER: IE
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US-08-469-318-70/c
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APPLICANT: Baston, Alan M.

APPLICANT: Xie.h, Barbara K.

APPLICANT: McKearn, John P.

APPLICANT: Olins, Peter O.

APPLICANT: Palk Kurnan

APPLICANT: Thomas, John W.

TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (I
                                                                                                                           0
                                                                                                                                                                              63 GGGCGGGGGGGGGGGGGGGCACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGC 122
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                            3 GCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAACAGAGGCCGGGAACG 62
                                                                                     Score 30; DB 3; Length 966;
Pred. No. 3.4;
                                                                                                                           80; Indeis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                         402 CGGGTTGATAGTAGAAITGGACCAGACGGTTCACCCG 365
                                                                                                                                                                                                                                                                                                 123 CGAATCTATAAAGGAACTAGTCCCGGCAAAAACCCCG 160
                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: ISM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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. Sequence 68, Application US/08468609A

. Pattent No. 6030812

. GENERAL INFORMATION:
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Braford-Goldberg,
                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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                                                                                         12.0%;
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nucleic acid
DEDNESS: double
                                                                            Query Match
Best Local Similarity 49.4%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P. O. Box 5110
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APPLICATION NUMBER: US
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     double
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RY: JSA
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STRANDEDNESS:
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APPLICANT:
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US-08-469-318-71
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Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (I 197\,
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                                                                                                                  522 GCCCIGGAICTICCICACTIGCTCTAAGCACTIGAGCAGGAAGCTCTGGGGCAGGGAGCT 463
                                            Gaps
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                                                                              3 GCCCCGGCTCCACGTGCTTTCTGCTGACTGACTGAACTACATAAACAGAGGCCGGGAACG 62
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      Length 966;
                                          80; Indels
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E: Corporate Patent Dept.
P. C. Box 5110
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APPLICATION DATA:
FILING DATF:
                                                                                                                                                                                                                                    123 CGAAICTATAAAAGGAACTAGTCCCGGCAAAACCCCG 160
                                                                                                                                                                                                                                                          402 CGGGTTGATAGTAGAGATTGGACCAGACGGTTCACCCG 365
  Score 30; DB 3;
Pred. No. 3.4;
                                          0; Mismatches
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REFERENCE/DOCKET NUMBER: C-2790/3
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-TBB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      Sequence 71, Application US/08468609A Patent No. 6030812
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Braford-Goldberg,
Caparon, Maire H.
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Klein, Barbara K.
McKearn, John P.
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    12.0%;
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TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 71
                                                                                                                                                                                                                                                                                                                                                                                                                              Abrams, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olins, Peter O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thomas, John W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 49.4
Matches 78; Conservative
                                            Conservative
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MEDIUM TYPE: Floppy
    Query Match
Best Local Similarity
Matches 78; Conserv
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USA
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US-08-468-609A-71/c
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ADDRESSEE:
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APPLICANT:
APPLICANT:
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STATE: II
COUNTRY:
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APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Caparon, Maire H.
APPLICANT: Caparon, Maire H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Dins, Peter O.
APPLICANT: Paik, Kunnan
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
                                                                                                0
                                                                                                                                                                                                                                    63 GGCCGGGGAGGAGGAGGACACAGGCTTTGACCGATAGTAACCTCTGCGGTGCGGGGCAGC 122
                                                                                                                                                          0; Gaps
                                                                                                                                  3 GCCCCGGCTCCACGTGCTTTCTGCTGACTGAACTACATAAACAGAGGCCGGGAACG 62
                                                      12.0%; Score 30; DB 3; Length 966; 49.4%; Pred. No. 3.4;
                                                                                                Indels
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STREET: P. C. Sox 5110
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATIVE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                80;
                                                                                                                                                                                                                                                                                      123 CCAATCTATAAAAGGAACTAGTCCCGGCAAAACCCCG 160
                                                                                                                                                                                                                                                                                                                        402 CGGGTTGATAGTAGAGTTGGACCAGACGGTTCACCCG 365
                                                                                              C; Mismatches
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FILING DATE: 14 FEB=1994
ATTORNEY/AGENT INPORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REPERENCE/DOCKET NUMBER: C-2790/3
TELECOMMUNICATION INFORMATION:
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06-JUN-1995
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MOLECULE TYPE: DNA (genomic)
MOLECULE TYPE: DNA (genomic)
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(314)737-6972
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Bauer, S. C.
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                              Conservative
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COMPUTER READABLE FORM:
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                                                                          Best Local Similarity
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                  US-08-468-509A-58
                                                                                            78;
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                                                          Query Match
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Search completed: February 3, 2003, 21:02:41 Job time: 25.7338 secs

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121 GCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCGTAATTGCGAGGGGAGGTCAG 180
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Sequence 3, Appli
Sequence 4, Appli
Sequence 817, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 1616, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8750, Ap
Sequence 320, App
                                                                                               (without alignments)
7959.555 Million cell updates/sec
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                                                                                 2003, 14:33:17 ; Search time 14.1109 Seconds
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1 gggccocggctccacgigct.....cagggcaggggggggggctc 250
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                                                                                                                                                                                                                                                                                                                                                                                                       1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NSW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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0 US-09-846-456-3

0 US-09-84-6-456-4

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0 US-09-747-810-1

0 US-09-747-1616

0 US-09-751-877-1

0 US-09-751-877-1

0 US-09-751-877-1

0 US-09-764-870-238

0 US-09-764-870-120

0 US-09-764-877-3062
                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                       US-09-596-141C-3_COPY_1394_1643
                                                                                                                                                                                                                                       396772 seqs, 224632407 residues
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                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_NA:*
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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length: 200000000
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Match Length DB
                                                      OM nucleic - nucleic search,
                                                                                 February 3,
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2893
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1704
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Sequence:
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Maximum DB seq
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31.2
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157.4
91
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No.
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Appl Appl Appl Appl Appli Appl	es Modifying	
Sequence 13, Sequence 12, Sequence 12, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 2, Paguence 4, Paguence 4, Paguence 5, Sequence 5, Sequence 5, Sequence 5, Sequence 3, Paguence 2, Paguence 1,	Cl Gene, Molecules Modifying	Length 3231;
0. US-09-119-042-13 0. US-09-119-042-13 0. US-09-119-042-11 0. US-09-119-042-11 0. US-09-119-042-11 0. US-09-119-042-10 0. US-09-119-042-8 0. US-09-119-042-8 0. US-09-119-042-7 0. US-09-119-042-7 0. US-09-119-042-7 0. US-09-119-042-7 0. US-09-119-042-7 0. US-09-119-042-8 0. US-09-119-042-8 0. US-09-119-042-8 0. US-09-119-042-8 0. US-09-119-042-8 0. US-09-119-042-9 0. US-09-9119-042-9 0. US-09-9119-042-9 0. US-09-9119-042-9 0. US-09-9119-042-9 0. US-09-9119-042-9 0. US-09-9119-042-1	ALIGNMENTS 6456 Nucleic Acid for the ABC1 and Therapeutic Uses 709/846,456 07201,280	Score 248.4; DB 10; Lo
0.000000000000000000000000000000000000	6-1 Vapplication US/098464 US2020146/92A1 PORMATION: Prodes, Catherine Lemoine, Catherine Lemoine, Laurent Denefie, Patrice Naudin, Laurent Denefie, Patrice Sewer, Bryan Frence, Silvia INVENTION: Regulatory N FRNCE: 3806.0505 FULCATION NUMBER: US/0 LICATION NUMBE	99.4%; larity 99.6%;
2000 2000 2000 2000 2000 2000 2000 200	ALIGNMENT 1S-09-846-456-1 Sequence 1, Application US/09846456 Patent No. US20020146792A1 GENERAL INFORMATION: APPLICANT: Pradae, Catherine APPLICANT: Pradae, Catherine APPLICANT: Denefile, Patrice APPLICANT: Remailey, Alan APPLICANT: Remailey, Alan APPLICANT: Regulatory Nucleic Aci TITLE OF INVENTION: Activity and Pherapeu TITLE OF INVENTION: Activity and Pherapeu TITLE OF INVENTION: Activity and Pherapeu TITLE OF INVENTION NUMBER: US/09/846,456 CURRENT FILING DATE: 2000-05-02 NUMBER OF SEQ ID NOS: 20 SEQ ID NO 1 TENET: DAA ORGANIEM: Homo Sapiens	Simi
)	RESULT 1 US-09-846 456-1 Sequence 1, A Sequent No. US GENERAL INFORM APPLICANT: APPLICAN	Query Match Best Local

CGGGGCGGGGAGGAGGAGCACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCA

9

1 GGGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAACAGGCCCGGGAA

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APPLICANT: Lillie, James
APPLICANT: Enrown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Van Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION: OF HUMAN CANCERS
GURRENT APPLICATION NUMBER: US/09/834,375
CURRENT APPLICATION NUMBER: 2001-64-13
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-64-14
NUMBER OF SEQ ID NOS: 1046
SOFTWARE: FastSEQ for Windows Version 4.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 CGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCT 226
                                                                                                                                                                                                                                                                                                                                                                                        160 GTAATTGCGAGCGAGGAGTGAGTGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCT 219
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 1704;
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Activity and Therapeutic Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.6%; Score 31.4; DE
llarity 61.7%; Fred. No. 1.5;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 CCGGCCTGCGGCAGGCCGGGGGGGGCTC 250
               FILE REFERENCE: 3806.0505
CURRENT APPLICATION NUMBER: US/09/846,456
CURRENT FILING DATE: 260--05-02
PRIOR APPLICATION NUMBER: US 60/201,280
PRIOR FILING DATE: 200-05-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PALGALIN VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CCGGCTGCGCCAGGCCAGGCGGGGGGGGCTC 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 817, Application US/09834975 Patent No. US20020110815A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)...(1704)
; OTHER INFORMATION: n = A,T,C or G
US-09-834-975-817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/09747810 ; Patent No. US20020012903A1
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                                                                                                                                                                                                                                                                                                                                             Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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LENGTH: 1704
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Best Local Simi
Matches 50;
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US-09-747-810-1
                                                                                                                                                                      SEQ ID NO 4
LENGTH: 221
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IITLE OF INVENTION: Regulatory Mucleic Acid for the ABC1 Gene, Molecules Modifying I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fojo, Silvia
TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying IT
TITLE OF INVENTION: Activity and Therapeutic Uses
FILE REFERENCE: 3806.0505
CURRENT APPLICATION WHBER: US/09/846,456
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/201,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 GCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCGIAATTGCGAAGCGAGAGTGAG 2914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.0%; Score 157.4; DB 10; Length 2893; 99.4%; Pred. No. 5.3e-40; tive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2855 GCCGAATCIATAAAAGGAACTAGTCCCGGCAAAACCCC 2893
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                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09846456 Patent No. US20020146792A1 GENERAL INFORMATION:
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; Sequence 4, Application US/09846455
; Patent No. US20020146792A1
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Naudin, Laurent
Denefie, Patrice
Duverger, Nicolas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.0
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APPLICANT: Rosier, Marie
APPLICANT: Prades, Catherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lemoine, Cendrine APPLICANT: Naudin, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Deneile, Patrice
APPLICANT: Duverger, Nicolas
                                                                                                                                                                                                                                                                                                                                                                                        Prades, Catherine
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APPLICANT: Remaley, Alan
APPLICANT: Fojo, Silvia
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Fojo, Silvia
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                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosier, Marie
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US-09-846-456-3
                                                                                                                                                                                         2975 CGGGGAGCTC 2984
                                                                                                                                                241 CGGGGAGCTC 250
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Matches 158; Conserv
                                                                                                                                                                                                                                                          RESULT 2
US-09-846-456-3
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APPLICANT:
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TGCGCTCGGTGCAGCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCCGTAATTGC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGAGGCCGGGAACGGGGCGGGGAGGGAGGGAGCACAGGCTTTGACCGATAGTAACCIC 107
                                                                                                                                 8629 CAGTGACCCATGCGCGCCTGCTCTCTCTGGAGGAGCTTCTTCTGGACTG 8686
                                                                                        170 GCGAGAGIGAGIGGGGCCGGGACCCGAGCCGAGCCGACCCITCICICCCGGGCTG 227
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Froteins, and Antibodies
FILE REPERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
PILOT application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2003
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.3%; Score 3C.8; DE 47.8%; Pred. No. 4.3; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                         Seguence 1616, Application US/09764847 Patent No. US20020132767A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09751877 Patent No. US20620142949A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 47.8°
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 81001
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRGANISM: Homo sapiens US-09-764-847-1616
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10275 CTGCAG 10280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 CGGCAG 233
                                                                                                                                                                                                                                                                                       US-09-764-847-1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1616
LENGTH: 10378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108
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      APPLICANT: Goldman, Steven A.
TITLE OF INVENTION: A METHOD FOR ISOLATING AND PURIFYING MULTIPOTENTIAL NEURAL PROGENITOR
TITLE OF INVENTION: CELLS AND MULTIPOTENTIAL NEURAL PROGENITOR CELLS
FILE REFERENCE: 19603/3280
CURRENT APPLICATION NUMBER: US/99/747,810
CURRENT FILING DATE: 2000-12-22
PRIOR FILING DATE: 1999-12-23
NUMBER OF SED ID NOS: 2
SED ID NO 1
LINGHH: 52216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30273 AAGTGGGAAGCATTCCAGGTAGGCGGGAGAGCAGGTGCAAAGGTCCTGAGGTAGGACTTA 30332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 GCTCGGTGCAGCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCGTAATTGCGAG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 AGGCCGGGAACGGGGCGGGGGGGGGGGGGCGACACGCTTTGACCGATAGTAACCTCTGC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 GAGGCCGGGAACGGGCGGGGAGGAGGAGACACAGGCTTTGACCGATAGTAACCTCTG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 CGCTCGGTGCAGCCGAATCTATAAAGGAACTAGTCCCGGCAAAAACCCCGTAATTGCGA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jength 52216;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
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Pred. No. 5.5;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/880,107 CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)..(10144)
OTHER INFORMATION: n = a or c or g or t
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PRIOR FILING DATE: 2000-60-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2168, Application US/09880107
Patent No. US20020142981A1
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51.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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US-09-747-810-1
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Best Local Similarity
-Loc 86; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 72; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-09-880-107-2168
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US-09-880-107-2168
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LOCATION: 1220..1238
OIHER INFORMATION: 20-828-311.mis
NAME/KEY: primer_bind
LOCATION: 1240..1258
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US-09-867-701-8750/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : polymorphic base C or
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OTHER INFORMATION: 17-41.rp complement
                                               CCCATION: 10946..12946
OTHER INFORMATION: 5'regulatory region
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LOCATION: 45863..45883
OTHER INFORMATION: 20-842.rp cc
NAME/KRY: primer_bind
LOCATION: 76644..76664
OTHER INFORMATION: 20-853.pu
NAME/KRY: primer_bind
LOCATION: 77166..77185
OTHER INFORMATION: 20-853.rp cc
NAME/KRY: primer_bind
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LOCATION: 45328..45347
OTHER INFORMATION: 20-642.pu
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NAME/KEY: primer_bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.rp
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                                                                                                                                               LOCATION: 12947..12958
OTHER INFORMATION: exon
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LOCATION: 42070..42090
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LOCATION: 15969..17969
              misc_feature
10946..12946
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LOCATION: 1239
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LOCATION: 15241
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DD 17479 GGGCTGCTCGTCCTCGCGCTGATGGGCCGGAACAGGTGATCAGGGGCAGGCGG 17420
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NAME/KEY: primer_bind
LOCATION: 45423..45441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: 20-842-115.mis complement NAME/KEY: priner_bind LAME/KEY: priner_bind COMEN: 77059.77057 OTHER INFORMATION: 20-853-415.mis
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LOCATION: 77059.77077
OTHER INFORMATION: 20-853-415.mis complement
                                complement
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NAME/KEY: primer_bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer_bind
LOCATION: 42219..42237
                                                                                                                                                                                   17-42-319.mis complement
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LOCATION: 12335..1235
COTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc. binding
LOCATION: 15229..1523
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc.binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
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LOCATION: 45430.45454
OTHER INFORMATION: 20-842-115.probe
LOCATION: 77046.77070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_binding
LOCATION: 1227..1251
OTHER INFORMATION: 20-829-311.probe
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LOCATION: 1240.1258
COTHER INFORMATION: 20-828-311.mis
OTHER INFORMATION: 20-828-311.mis
NAME/KEY: primer_bind
LOCATION: 12328..12346
OTHER INFORMATION: 17-42-319.mis
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                                                                                                                                                                                                                           LOCATION: 15222..1524v
COTHER INFORMATION: 17-41-250.mis
NAME/KEY: priner_bind
rocation: 15242..15260
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                                                                                                                           NAME/KEY: Primer_bind
LOCATION: 12348..12365
OCHER INFORMATION: 17-42
NAME/KEY: Primer_bind
LOCATION: 15222.15240
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LOCATION: 45443..4546
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Molnar, Istvan
Zirkle, Ross
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APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
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ORGANISM: Homo sapiens
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LENGTH: 2219
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                                                                                                                                                                                                                                                                                             Length 289;
               APPLICANT: Jones, Robert
APPLICANT: Harlocker, Subert
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.437
CURRENT APPLICATION NUMBER: US/09/867,701
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8750
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT APPLICATION NUMBER: US/09/925,300
FILE APPLICATION NUMBER: PCT/US00/05988
PRIOR PAPLICATION NUMBER: PCT/US00/05988
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PRILING DATE: 1999-03-12
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                                                                                                                                                                                                                                                                                          DB 10;
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                                                                                                                                                                                                                                                                                          11.8%; Score 29.6; 50.0%; Pred. No. 3;
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OTHER INFORMATION: n equals a,t,g, or
NAME/KBY: misc feature
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Patent No. US20020151681A1
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OTHER INFORMATION: n equals a,t,g,
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SOFTWARE: Patenil: Ver. 2.0
SEQ ID NO 320
LENGTH: 1756
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APPLICANT: Aglate, Paul A.
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CONGANISM: Homo sapien
US-09-867-701-8750
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Matches 47; Conserv
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Best Local Similarity
Matches 74; Conserv
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US-09-925-300-320/c
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                                               182 GGGMTGCTGCTCCTCGTCCTCGCCGTGATGGGCCGGAACAGGTGATCAGGGGCAGGCGG 123
GGGCCCGGGCTCCACGTGCTTTCTGCTGACTGAACTACATAAACAGAGGCGGGAA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 646 SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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Pred. No. 19;
0; Mismatches
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CURRENY APPLICATION NUMBER: 0S/16/014,717
CURRENY FILING DATE: 2001-111-13
PRIOR APPLICATION NUMBER: US/09/335,409
PRIOR FILING DATE: 1999-06-17
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CURRENT APPLICATION NUMBER: US/09/764.870
CURRENT FILING DATE: 2001-01-17
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; Sequence 238, Application US/09764870
; Patent No. US20020042386A1
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OTHER INFORMATION: n equals a,t,g,
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Best Local Similarity 61.8%;
Matches 47; Conservative
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                                            Gaps
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11.8%; Score 29.4; DB 10; Length 2219; 56.8%; Pred. No. 7;
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al.
TITLE COF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT21.
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
PLOT APPLICATION GATE removed - consult PALM or file wrapper NUMBER OF SED ID NOS: 646
SOFTWARE: Patent:: Ver. 2.0
SED ID NO 120
LENGTH: 2272
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CURRENT FILING DATE: 2001-01-17
Prior application date removed - consult PAIM or file wrapper NUMBER OF SEQ ID NOS: 2003
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                                            0; Mismatches 41;
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ilarity 47.3%; Pred. No. 14;
Conservative 0; Mismatches
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Matches 54; Conservative
                                              54; Conservative
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US-09-764-847-1615
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 88; Conserv
    Query Match
Best Local Similarity
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US-09-764-870-120/c
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LENGTH: 1047
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APPLICANT: SHIBAMAA, SHIRO
APPLICANT: TADA, HIDEAXI.
TILE OT INVENTION: THE BOTH
FILLE REPERENCE: G58769
CURRENT APPLICATION NUMBER: US/09/529,063
CURRENT APPLICATION NUMBER: PCT/JP98/04514
PRIOR PPLICATION NUMBER: PCT/JP98/04514
PRIOR APPLICATION NUMBER: JP 9-274674
PRIOR APPLICATION NUMBER: JP 9-274674
PRIOR FILLING DATE: 1998-10-06
PRIOR FILLING DATE: 1998-10-06
PRIOR FILLING DATE: 1998-10-06
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                                                                       108 IGCGCTCGGTGCAGCCGAATCTATAAAGGAACTAGTCCCGGCAAAAACCCCGGTAATIGC 167
                                                                                                                                                                            GAGCGAGAGIGAGIGGGGCCGGGACCCGCAGAGCCGAGCCGACCCIICICICCCGGGCTG 227
                                                                                                       Length 2796;
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58.0%; Pred. No. 12;
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 51, Application US/09529063
Patent No. US20026102542A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.5
Best Local Similarity 58.0
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: sig_peptide
LOCATION: (11)..(58)
NAME/KEY: mat_peptide
LOCATION: (59)..(1273)
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (11)..(1273)
US-09-529-063-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                               5619 CIGCAG 5624
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US-09-529-063-51/c
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LENGIH: 2796
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Sequence 994, App
Sequence 14, Appl
Sequence 3972, Ap
Sequence 4299, Ap
Sequence 19, Appl
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Sequence 2064, Ap
Sequence 351, App
Sequence 453, App
Sequence 192, App
Sequence 192, App
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Sequence 1, Appli
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Sequence 255, App
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Sequence 8332, App
Sequence 8332, App
                                                                                     3, 2003, 14:33:17 ; Search time 86.4714 Seconds (without alignments) 7959.555 Million cell updates/sec
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/cgn2_6/ptodata/1/pubpna/PCT_NBW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCT_NBW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_NBW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_PUBCCMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUB_PUBCCMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUB_PUBCCMB.seq:*
/cgn2_6/ptodata/1/pubpna/USOB_NBW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USOB_NBW_PUB.seq:*
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-925-301-351
US-09-834-975-453
US-09-731-872-192
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US-09-860-670-255

US-09-860-670-260

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US-09-443-704-19
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Listing first 45 summaries
                                                           - nucleic search, using sw model
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Perfect score:
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9-800-729-4	9-764-846-3	-09-764-846-10	-09-864-864-16	-729-674-14	-764-870-61	-09-764-870-61	64-869-1	-09-925-301-54	19-834-975-79	-09-992-598	-09-989-293A-2	-09-989-735-29	-09-990-444-29	-09-989-730-29	-08-980-436-29	-09-991-181-29	1-953-687-29	-09-989-734-29	-09-997-653-29	-10-174-590-21	10-176-758-21	-10-175-737-21	-09-989-722-29	23-2	-09-989-279-29
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ALIGNMENTS

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APPLICANT: FOUR SILVIA
TITLE OF INVENTION: Regulatory Nucleic Acid for the ABCI Gene, Molecules Modifying
TITLE OF INVENTION: Activity and Therapeutic Uses
FILE REFERENCE: 3806.0505
CURRENT APPLICATION NUMBER: US/09/846,456
CURRENT APPLICATION NUMBER: US 60/201,280
PRIOR APPLICATION NUMBER: US 60/201,280
PRIOR FILING DATE: 2000-05-02
SOFIWARE: Patentin version 3.0
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97.9%; Pred. No. 0;
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                      Sequence 3, Application US/09846456
Patent No. US20020146792AL
GENERAL INFORMATION:
                                                                                                                                                                          Duverger, Nicolas
Brewer, Bryan
Remaley, Alan
Fojo, Silvia
                                                                                                                   Lemoine, Cendrine
Naudin, Laurent
                                                                          APPLICANT: Rosier, Marie
APPLICANT: Prades, Catherine
                                                                                                                                                           Denefle, Patrice
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Matches 1504; Conservative
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US-09-846-456-3
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1525 ATGATGGAGCTGGAGGTGGGAAGAAGTAGGCTTGGGGCAGCTCTCTCATGCCACCTCA
                                                                                                                       TTCTGGCCAAAACTCAGGTCAAACTGTGAAGGTCTAAATGTGAATCTGCCCTTCAAGGT
                                                                                                                                                    GGCTACAAAGGTATCTTTGTCAAGGTAGGAGACCTTGTGGCCTCCACGTGCACTTCCAGG
                                                                                                                                                                                                       372 GCCTGCTT-GGCCTCTTCTACGGGTCTGTCCTGAGTCTTCTATGAATCTCCCTTCAGGGC
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                                                                                               TICTEGCCAAAACTCAGGTCAAACTGTGAAGAGTCTAAAATGTGAAATCTGCCCTTCAAGGT
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APPLICAMY: Practs, Catherine
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APPLICAMY: Deverger, Nicolas
APPLICAMY: Brewer, Nicolas
APPLICAMY: Remaley, Alan
APPLICAMY: Fojo, Silvia
TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying
TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying
TITLE OF INVENTION: Activity and Therapeutic Uses
FILE REFERENCE: 3006.0505
CURRENT APPLICATION NUMBER: US 60/201,280
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                                                   1262 GCCCGGGCGGGGAAGGGGACGCAGACGCGGACCCTAAGACACCTGCTGTACCCTCCAC 1321
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                                                                                           2598 GCCGGGCGGGGGAAGGGAACCCAGCACCGCGGACCTAAGACACCTGCTGCTGCTCCAC
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Patent No. US20020146792A1
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Matches 1504; Conservative
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APPLICANT: Rosier, Marie
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ORGANISM: Homo sapiens
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CCCTGCTT-GGCCTCTTCTACGGGTCTGTCCTGAGTCTTCTATGAATCTCCTTCAGGGC
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Patent No. US20020146792A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.0
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APPLICANT: Rosier, Marie
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||582 AGGTGGCAT
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APPLICANT: Adjate, Paul A.
APPLICANT: Adjate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIACNOSIS AND THER
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIACNOSIS AND THER
TITLE OF INVENTION: COMPOSITIONS OF COMPOSITIONS AND THER
TITLE OF INVENTION: COMPOSITION OF COM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prior application data removed - consult PALM or file wrapper NUMBER OF SED ID NOS: 289
SOFTWARE: Patentim Ver. 2.0
SEQ ID NO 260
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ruben et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA12791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/660,670 CURRENT FILING DATE: 2001-05-21
                                                                                                                TTTCTTTTTTGTGTGCCTCCTTCCTCT
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Publication No. US20020198362A1
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FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                       Sequence 260, Application US/09860670 Patent No. US20020165137A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-09-860-670-260
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APPLICANT: Remalley, Alan
APPLICANT: Remalley, Alan
TITLE CAINVENTION: Activity and Therapeutic Uses
TITLE OF INVENTION: Activity and Therapeutic Uses
TITLE OF INVENTION: Activity and Therapeutic Uses
CURRENT APPLICATION NUMBER: US/09/846,456
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/201,280
NUMBER OF SEQ ID NOS: 20
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Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 289
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PALSTYPIN
CURRENT APPLICATION NUMBER: US/09/860,670
CURRENT FILING DATE: 2001-05-21
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66.7%; Pred. No. 0.51;
ative 0; Mismatches 31;
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65.9%; Pred. No. 2.2e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn version 3.0
                                                      Prades, Catherine
Lemoine, Cendrine
Naudin, Laurent
                                                                                                                                        Denefle, Patrice
Duverger, Nicolas
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GENERAL INFORMATION:
APPLICANT: Rosier, Marie
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SEQ ID NO 255
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Query Match
Best Local Similarity 68.77
Matches 57; Conservative
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US-09-834-975-994
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Matches 65; Conserv
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US-09-764-877-3972
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                                                                                                                                                                                                                                                                                                                                                 Length 366;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PAILO
CURRENT APPLICATION NUMBER: US/09/764,855
CURRENT FILING DAIE: 2001-01-17
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65.6%; Pred. No. 0.089;
tive 0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                               Score 43; DB 9;
Pred. No. 0.053;
                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SCFWRARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8332
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Patent No. US20020110815al
GENERAL INCORMATION:
APPLICANT: LILLIE, James
APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrew
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Patent No. US20020119919A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          LOCATION: (255)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                               2.8%;
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NAME/KEY: unSure
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Best Local Similarity 65.68
Matches 61, Conservative
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Best Local Similarity 65.6*
Thes 61; Conservative
                                                                                                                                                        IYPE: DNA
ORGANISM: Homo sapiens
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US-09-764-855-60
                                                                                                                                                                                                            NAME/KEY: unsure
                                                                                                                                                                                                                                                                                               ; OTHER INFORMAT:
US-09-796-692-8332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-764-855-50/c
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APPLICANT: Van Euffel, Christophe TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS ITLLE OF INVENTION: NOVEL GENES, COMPOSITION, ASSESSMENT, PREVENTION, AND THERAPY ITLLE OF INVENTION: OF HUMAN CANCERS
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ 1D NOS: 646
SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2001-11-17
Prior application data removed - refer to Falm or file wrapper
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT214
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC005
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62.5%; Pred. No. 0.32;
tive 0; Mismatches 39;
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68.7%; Pred. No. 0.38;
tive 0; Mismatches 26;
                                                                                      FILE REFERENCE: MAI-016
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DAIE: 2001-04-13
FRIOR APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 994
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; Patent No. US20020147140A1
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TYPE: DNA
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APPLICANT: Law Rosa, Thomas J.
APPLICANT: Law Rosa, Thomas J.
APPLICANT: Law Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with TITLE OF INVENTION: Plants
FITLE OF INVENTION: Plants
FILLE REFERENCE: 38-21(15401.)8
CURRENT APPLICATION NUMBER: US/09/878,574
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILLING DATE: 1999-06-14
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LOCATION: (1)..(545)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone LD: LIB3028-013-Q1-H1
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50.2%; Pred. No. 1.3;
tive 0; Mismatches
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PRIOR APPLICATION NUMBER: 60/109,294
                                                                                                                                                      Query Match
Best Local Similarity 60.2%
Matches 68; Conservative
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
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US-09-764-877-3972
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LENGTH: 545
                  SOFTWARE: Pat
SEQ ID NO 3972
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APPLICANT: Liu, Zhan-Bin
APPLICANT: Cathoon, Rebecca E.
APPLICANT: Cathoon, Rebecca E.
APPLICANT: Gall, Joan
APPLICANT: Gafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Wang, Zude
TITLE OF INVENTION: Plant MYB-Related Transcription Factors
FILE REFERENCE: BB1280 US NA
CURRENT FILING DATE: 1999-11-19
EARLIER APPLICATION NUMBER: G0/109,294
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Office 97
SEQ ID NO 19
SEQ ID NO 19
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TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEO ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
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60.6%; Pred. No. 0.63;
live 0; Mismatches
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Patent No. US20020061521A1
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Patent No. US20020065120A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Offlice 97
SEQ ID NO 19
LENGTH: 1372
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Best Local Similarity
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Best Local Similarity
                                                                                                                             ; ORGANISM: Zea mays
US-10-008-118A-19
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CRGANISM: Zea mays
US-09-443-704-19
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AC126316 AC121553 N AC121553 N AC127041 P AC114705 P AC117126 B AC126984 P

PRI 10-APR-2001 Bukaryota: Metazoa: Chordata; Craniara; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primares; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1167) Porsch-Ozcurumez,M., Langmann,T., Heimerl,S., Borsukova,H., Kaminski,W.E., Drobnik,W., Honer,C., Schumacher,C. and Schmitz,G. HSA252201 1167 bp DNA linear PRI: Homo sapiens partial ABC-1 gene for ATP-binding cassette transporter-1, 5'UTR and promoter region. ABC-1 gene; ATP-binding cassette transporter-1; promoter AJ252201.1 GI:12053757 Homo sapiens human, DEFINITION ORGANISM HSA252201 LOCUS ACCESSION VERSION KEYWORDS SOURCE AUTHORS REFERENCE RESULI

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The zinc finger protein 202 (ZNF202) is a transcriptional repressor of ATP binding cassette transporter A1 (ABCA1) and ABCG1 gene expression and a modulator of cellular lipid efflux 2. Biol. Chem. 276 (15), 12427-12433 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                               IGOGGAAAGCAGGAITITAGAGGAAGCAAAITCCACTGGIGCCGITGGCTGCCGGGAACGT
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/function="cholesterol efflux regulatory protein"
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100.0%; Pred. No. 5.8e-125;
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/cell_type="leukocyte"
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Porsch-Oezcueruemez,M.K.
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                                                                                                                                                                                                                                                                                             /gene="ABC-1"
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                                                                                            AUTHORS
TITLE
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae: Homo.
1 (bases 1 to 1643)
Lewn, R.M., Wade, D. and Garvin, M.
Regulation with hinding cassette transporter protein abcl
Patent: WO 0078972-A 3 28-DEC-2000;
CV TEBRAPEUTICS, INC. (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAGCTCICTCTCCCCCCAAICCCTCCCTCCGGCTGAGGAAACTAACAAAGGAAAAAAAT
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                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 564; DB 6; I Best Local Similarity 100.0%; Pred. No. 5.8e-125; Matches 564; Conservative 0; Mismatches 0;
                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                       403
                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
413 c 457 q 403
                                                                                       Sequence 3 from Patent WO6078972.
AX060715
AX060715.1 GI:12406104
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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LOCUS

AXC60894

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AUTHORS

REFERENCE

JOURNAL

source

FEATURES

BASE COUNT

ORIGIN

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corresponding to the overlapping clone, as we submit sequences with only a small everlap as described above.

In sequence was finished as follows unless otherwise noted: all regions were either double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EM3: Sw:, SWISSPROT, Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping the contraction of the worm of the contraction of the contractio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMPORTANT: This sequence is not the entire insert of clone RPII-21787 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true right end of clone RPII-21787 is at $6717 in this sequence. The true left end of clone RPII-122F10 is at 72980 in this sequence. The true right end of clone RPII-132F10 is at 2000 in this sequence.
                                                                                                                                                                                                                                                                                             Submitted (11-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgesiire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Jan 15, 2002 this sequence version replaced gi:18121468.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/HGB/Chrg
RPI1-217B7 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chci.org/bacpac/home.htm
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Institutes of Heath, National Heatt, Lung and Blood
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84249. .84273
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Pred. No. 6.2e-125;
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/db_xref="taxon:9606"
/chromosome="9"
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3238. .3278
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21138 c 20380 g 2
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GI:18151453
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ORIGIN
                                                                                                  ORGANISM
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JOURNAL
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                                   KEYWORDS
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Human DNA sequence from clone RPI1-217B7 on chromosome 9, complete
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Marmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1643)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 Tecegaaagcaggatttagaggaagcaaattccactggccccttggctgccgggaacgt 120
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Atp binding cassette transporter protein abol polypeptides
Patent: Wo 0078971-A 3 28-DEC-2003;
CV THERAPEUTICS, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1643;
                                   linear
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Pred. No. 5.8e-125,
0; Mismatches 0;
                                   DNA
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                     Sequence 3 from Patent WO0078971.
AX060894
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/db_xref="taxon:9606"
( 413 c 457 g 403
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100.0%;
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Best Local Similarity 100.(
Matches 564; Conservative
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AL359182
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Length 96717;

DEFINITION AL359182/C

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Direct Submission
Submitted (21-07-1999) Whitehead Institute/MIT Center for Genome
Research, 520 Charles Street. Cambridge, MA 02141, USA
On Apr 22, 2000 this sequence version replaced gi:6454033.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. Tris record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consensus quality: 117571 bases at least 040 consensus quality: 145749 bases at least 030 consensus quality: 160940 bases at least 020 lisert size: 185000; agarose-fp tisert size: 171264; sum-of-contigs quality coverage: 2.9 in 020 bases; sum-of-contigs quality coverage: 5.2 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13: M77815; 100% of reads
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.960731
                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seg.wi.mit.edu
Contact: seguence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp
of 1270 bp in length
100 bp
of 1994 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 1531 bp in length 100 bp of 1681 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25/00 2000: ...
25808 28184: gap of 100 bp
28185 28284: gap of 100 bp
28185 31338: contig of 3054 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9786: gap of 100 bp
12253: contig of 2467 bp in length
12353: gap of 100 bp
15328: gap of 100 bp
15328: gap of 100 bp
17209: contig of 1872 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20231: gap of 100 by 22587: contig of 2356 bp in length 22687: qap of 100 by 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42836 42935: gap of 100 bp 42936 45448: contig of 2513 bp in length 45449 4548 ap of 00 bp 45549 48116: contig of 2568 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 1003: contig of 1003 bp in length
1004 1103: gap of 100 bp
1104 2634: contig of 1531 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 bp .
f 1707 bp in length
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2377 bp in length
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Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 bp
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5785: contig of
5885: gap of 10
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9686: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: L2510
Center clone name: 1_M_10
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38318: cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12254 12353: gap of 152354 15228: conf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2635 2734: gap of
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                                      TITLE
JOURNAL
                                                                                                                                                                COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boquslavkiy, L., Boukhgalter, B., Brown, A. Castle, A., Colingelo, M., Collins, S., Collywcre, A., Cooke, P., DeArellano, K., Dewar, C. Domillo, M., Donelan, L., Doyle, M., Perreira, P., Fitziugh, W., Forrest, C., Funke, R., Gaqe, D., Galagan, J., Gardyna, S., Græbt, G., Fanke, R., Horton, L., Howland, J., Cardyna, S., Græbt, G., Fann, E., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Peterson, K., Pollara, V., Riban, C., Rann, C., Corono, T., O'Donnell, P., Peterson, K., Pollara, V., Riban, R., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
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1-1M10, WORKING DRAFT SEQUENCS, 39 unordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CIGCGCTCGGTGCAGCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCCGTAATTG 17251
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                                                                                                                                                                                                                                                                              301 CCCGTTTAAGGGGCGGGCCCCGGCTCCACGTGCTTICTGCTGAGTGACTGAACTACATAA 360
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C; Mismatches
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Matches 564; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 CCGITTAAGGGGGGGCCCGGCTCCACGTGCTTCTGCTGAGTGACTGAACTACATAA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGAGCGAGAGTGAGTGGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TGCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GGACTAGAGAGTCTGCGGCGCAGCCCCGAGCCCAGCGCTTCCCGGGGGTCTTAGGCCGGC
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100.0%; Score 564; DB 2; I
Best Local Similarity 100.0%; Pred. No. 6.3e-125;
Matches 564; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                         /note="assembly_fragment"
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/note="assembly_fragment"
45549. 48116
/note="assembly_fragment"
48217. 55518
/note="assembly_fragment"
52719. 56592
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56693. .59635
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/note="assembly_fragment"
63762. .68437
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68538. .71459
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/note="assembly_fragment"
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38419. .42835
/note="assembly_fragment"
31439. .34299
/note="assembly_fragment"
34400. .38318
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/note="assembly_fragment
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71559. .76888
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                                                                                                                                                                                                                                                                                                                                                              gap of 100 bp in length 58: contig of 2921 bp in length gap of 100 hr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71558: gap of 100 bp 76888: contig of 5330 bp in length 76988: gap of 100 bp 8213: contig of 5125 bp in length 82213: gap of 100 bp 82220: contig of 6007 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3116: gap of 100 bp 109181 control of 10918 control of 10928 in length 100 bp 278; gap of 100 bp 20 12307; control of 8029 bp 2n length
p of 100 bp
contig of 4402 bp in length
p of 100 bp
contig of 3874 bp in length
                                                                                                                                                      p of 100 bp contig of 2943 bp in length p of 100 bp contig of 3926 bp in length
                                                                                                                                                                                                                                                                                                                61: gap of 100 bp
68437: contig of 4576 bp in length
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97901: contig of 4302 bp in length
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/note="assembly_fragment"
20232. .22587
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1104. .2634
/note="assembly_fragment"
2735. .4415
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1516. .5785
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9787. .12253
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2354. .15228
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15329, .17200
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'note="assembly_fragment"
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25608. .28184
/note="assembly_fragment"
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7980. .9686
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/db_xref="taxon:9606"
48216: gap of
52518: contig
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.u. gap of
63661: r.
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59635: c
59735:
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71458: cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-JUN-2006) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San
Francisco, CA 94143-0130, USA
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Ullingers 1 co. 1167)

Bullinger C.R., Hakamata, H.D., Duchateau, P.N., Eng, C.,
Analysis of habol gene 5' end: additional peptide sequence,
promoter region, and four polymorphisms

Diochem. Biophys. Res. Commun. 271 (2000) In press

(bases 224 to 1167)

Ullinger C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Anuizara, B.E. ? Aleiding, C.J. and Kane, J.P.,
Direct Submission
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On Jun 23, 2000 this sequence version replaced gi:7769713.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Exteleostomi;

I (bases 1 to 18399;)

Hayden, M.R., Brooks Wilson, A.R., Pimstone, S.N. and Clee, S.M.

Compositions and methods for modulating hdl cholesterol and trigityceride levels

Patent: WO 0115676-A 1 08-MAR-2001;

University of British Columbia (CA); Xenon Genetics Inc. (CA)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATAAACAGGCCGGGAACGGGGGGGGGAGGAGGGAGGCACAGGCTTTGACCGATAGT 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGT
                    754 CCCGITTAAGGGGCCCCCGGCTCCACGTGCTITCTGCTGAGTGACTGAACIACATAA
                                                            361 ACAGAGGCCGGGAACGGGGGGGGGGGAGGGAGGCACAGGCTTTGACCGATAGTAACCT
                                                                                     CTGCGCTCGGTGCAGCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCGGTAATTG
                                                                                                                                                                      28372 TGCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGACTAGAGAGTCIGOGGCGCAGCCCGGAGCCCAGCGCTTCCCGGCGCGTCTTAGGCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28432 GGACTAGAGAGTCTGCGGCGCAGCCCCGAGCCCAGCGCTTCCCGCGGGTCTTAGGCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 A----COCCCACCCCACCCACCTCCCCCAACTCCCTAGATGTGTCGTGGGCGGCTGAA
PAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
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/db_xref="taxon:9605"
49549 a 37944 c 41170 g 54950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1 from Patent W00115676.
                                                                                                                                                                                                                                                                                                                                           GCGGCAGGGCAGGCGGGGAGCTC 1017
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Tue Feb

PRI 17-JUL-2000

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/organism="Homo sapiens"
/db_xref="taxon:9606"
1454. 148834
/ds.xon:9606"
1454. 148834
/gene="Abana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

[ bases 1 to 149034)

Santamarina-Fojo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L.,
Cheng,J.F., Osorio,J., Remaley,A., Yang,X.P., Haudenschild,C.,
Prades,C., Chimini,G., Blackmon,E., Francois,T., Duverger,N.,
Rubin,E.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete genomic sequence of the human ABCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000) 20345099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 149034)
Santamarina-Pojo/S., Peterson,K.M., Knapper,C.L., Freeman,L.A.,
Remaley,A.T., Yang,X.-P., Haudenschild,C.C., Blackmon,E.E.,
Francois,T.L. and Brewer,H.B. Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-JUN-2006) Molecular Disease Branch, National Institutes of Heath, National Heart, Lung and Blood Institute, Bethesda, MD 20892, USA
          2836 AACTCTGGGCTGGTGCAGCGGAATCTATAAAAGGAACTAGTCCCGGCAAAAAACCCCGT
                                                                                                         476 AATIGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGGCGGAGCCGACCCTTCTCTCCC
                                                                                                                                                                                                                                                                                                                                                  linear
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/gene="ABCA1"
                                                                                                                                                                                                        2956 GGGCTGCGGCAGGGCAGGCGGGGGGGGTC 2984
                                                                                                                                                                             GGGCTGCGCCAGGCCAGGGGGGGGGCTC 564
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4240. .4509
/rpt_family="Alu"
4998. .5270
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AF275948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P., Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S. Regulatory nucleic acid sequences of the abol gene Paten: WO 0163746-A 1 08-NOV-2001;
                                                                                                                                                                                         28731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2416 GAGCTCTCTCTCCCCCAICCTCCCTCCGGCTGAGGAACTAACAAAAAAAT 2475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2476 TGCGGAAAGCAGGATTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAAGGT 2535
                                                                                                                                                                        535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GGGCCGGGGGGGAAGGGGACGCAGACCGCGGGACCCTAAGACACCTGCTGTACCCTCC 240
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                                                                             475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TCCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAAGGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 CGTCGCCCGTTTAAGGGGGGGGCCCCGGCTCCCACGTGCTTTCTGCTGAGTGACTGAACTA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACCTCTGCGCTCGGTGCAGCCGAATCTATAAAGGAACTAGTCCCGGCAAAAACCCCGT 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAGCTCTCTCCCCCCAATCCCTCCCTCCGCCTGAGGAAACTAACAAAGGAAAAAAA 60
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                                                                                                                                                                     Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 5.7e-121;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1 from Patent WC0183746.
AX351029
AX351029.1 GI:18616385
                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 98.9°
Matches 563; Conservative
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AX351029
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RILDGGGQNDILEIKELTKIYRRKRKPAVDRICVGIPPGBCFGLLGVNGAGKSSTFKM
LIGDTTVIRGDAFLNXNSILSNIHEVHONMCYCPOFDAITELLIGREHVEFFALLRGV
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  KSYVSSTNLPVLALLLLLYGWSTTPEMYPASFVFKIPSTAYVVLTSVNLFIGINGSVA
TFVLELFTDNKLNNINDILKSVFLIFPHFCLGRGLIDKYKNQAMADALERFGENRFVS
                                                PLSWDLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQ
                                                                                                                  PEKEVGKVGEWAIRKLGLVKYGEKYAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTG
                                                                                                                                      MDPKARRFLWNCALSVVKEGRSVVLISHSMEBCEALCTRMAIMVNGRFRCLGSVQHLK
NRFGDGYTIVVRIAGSNPDLKPVQDFFGLAFPGSVXKEKHRNMLQYQLPSSLSSLARI
                                                                                                                                                                                    FSILSQSKKRLHIEDYSVSQTTLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLT
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Pred. No. 6e-121;
0; Mismatches 1;
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/gene="ABCA1"

/note="A009x28"

41593. 41835

/rpt_family="Alu"

/1557. 41679
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/rpt_family="Alu"
55029. .55774
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44349, .44626
/rpt_family="Alu"
48473, .48669
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54285. 54418
/rpt_family="Alu"
54849. 54988
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37617. 37892
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NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAXMTTSVDVLVSICVIFAMSFV
PASFVVFLIQERVSKAKHLQFISGVKPVITMLSNFVMDMCNYVVPATLVIIIFICFQQ
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SWSDMRQEVMFLINVNSSSSSTQIYQAVSRIVCGHPEGGGLKIKSLNWYEDLF
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QQLDGLDWTAQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNQAIRTISRFMECVNLN
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DGTLPARRNRRAFGGXQSCLRPFTEDDAADPNDSDIDPESRETDLLSGMDGKGSYQVK
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LQPWYNEQYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQAGEEEW
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SYPPYEQHECHFPNKAMPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIV
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NJSLPKSTVDXMLRADVIJHKVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLP
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SQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLKYRGGRTIILST
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Homo sapiens ATP-binding cassette 1 sub-family A member 1 (ABCA1)
and SNAP protein genes, complete cds.
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                                                                                             TGCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAAGGT 1095
                                                                                                                                                                                1336 CATAAACAGGCCGGGAAGGGGGGGGGGAGGAGGGAGGAGCACAGGCTTTGACCGATAGT 1395
                                    GAGCTCTCTCCCCCAATCCCTCCCTCCGGCTGAGGAAACTAACAAAGGAAAAAAAT 1035
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GASCICICICICCCCCAAICCCTCCCTCCGGCTGAGGAAACIAACAAAGGAAAAAAAA
                                                                              IGCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 201144)
Qiu,Y., Caveller,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
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Mammalia, Butheria, Primates,
1 (bases 1 to 201144)
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KEYWORDS
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.72986,77520. .77661,78931. .73649,
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LQPWMYNBQYTFVSNDAPBDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQAGEEEW
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DILQOLIGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQEVN
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KEKLAAABRYLRSNMDILKPILRILNSTSPFPSKELABAIKTLLHSLGTLAQELFSMR
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RQVMAEVNKTFQELAVFHDLEGMWEELSPKIWTFMENSQEMDLVRMLLDSRDNDHFWE
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KLEPTAT EVWLINKSMELLDERKFWAGIVFTGITPGSIELPHHVKYKIRMDIDNVERT
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PCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIKGIVYEKEARLKEIMRIMGLDNSILM
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NAIILRANLQKGENPSHYGITAFNHPINLTKQQLSEVALMTTSVDVLVSICVIFAMSFV
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/protein_id="AAX43526.1"
/db_xref="GI:13876613"
/translation="MACWPQLRILLWKNLTFRRRQTCQ5LLEVAWPLFIFLILISVRL
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ARLFSDARRILLLYSQXDTSMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYH
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101048. 101169,104152. 104328,117287. 117379,
122329. 122569,125285. 125424,125754. 127379,
133079. 133030,135677. 135898,136959. 1371749. 131925,
133708. 133930,135677. 135898,136959. 137163,
13868. 138381,140779. 140350,141340. 141471,
142777. 142919,142132. 14260,143963. 144183,
145477. 145519,145677. 146859,148577. 148575,
148771. 146844,150380. 156428,15278. 152202,
159482. 159714,160837. 166942,165788. 166703,
166815. 166959,168905. 168628,165788. 166703,
170498. 174589,174961. 177619,178960. 178709)
122329. 122569,125285. 125424,125754. 125870,130079. 130276,131023. 131228,131749. 131925,133708. 133300,135677. 125898,1335659. 137163,138268. 13838,1140179. 140350,143963. 144183,142777. 142919,143123. 143260,143963. 144183,14577. 142919,143123. 146859,148527. 148575,146771. 148884,150280. 150428,152078. 152202,153488. 155568. 156757,156828. 156757,156828. 166793,163182,16413. 164990,16588. 166703,
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176142,
1. 181457)
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.76625. .176717,177376.
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/number= 14541. /qene="x /number= 146657. /gene="x /number= /gene="x /gene="x /gene="x	eXOn		/gene="A /pumber= 153438.	757	Query Match 95.9%; Score 541; DB 9; Length 201144; Best Local Similarity 98.2%; PreG. No. 2.1e-119; Matches 559; Conservative 0; Mismatches 5; Indels 5; Gaps 1;	QY 1 GAGCTCTCTCTCCCCCATCCCTCCGCTGAGGAACTAACAAAGGAAAAAAAA	QY 61 TGCGGAAAGCAGGATTTAGAGGAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGT 120 	QY 121 GGACTAGAGAGTCTGCGGCGGCAGCCCCAGCGCTTCCCGCGCGTCTTAGGCCGGC 180 DD 33573 GGACTAGAGAGTCTGCGGCGAGCCCCGAGCGCTTCCCGCGCGTCTTAGGCTGGC 33532	QY 181 GGGCCCGGGCGGGGAAGGGGACCCAACCGCGGACCCTAAGACACCTGCTGTACCCTCC 240 Db 33633 GGGCCCGGGCGGGGGAAGGGCACGCAGGACCCGGAACACCTAAGACACCTGCTGTACCCTCC 33692	OY 241 ACCOCCACCCCACCCACCCCCCCACTCCCTGAGTGTCGTGGCGGCTGAA 295	OY 296 CGICGCCGTTTAAGGGGCGGCCCGGCTCCACGTGCTTTCTGGTGACTGAC	QY 356 CATAAACAGAGGCCGGGAACGGGGGGGGGGGGGGGGGGG	QY 416 AACCTCTGGGCTCGGTGCAGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCGGT 475 Db 33873 AACCTCTGCGCTCGGTGCAGCAATCTATAAAAGGAACTAGTCTGGGCAAAAACCCGT	ON 476 AATTGCGAGCGAGCGAGGCCGGGACCCCCAGACCGAGCCGACCCTTCTCTCCC 535	9y 536 GGCTGCGCAGGCGGCGGAGCTC 564	RESULT 11 AC021246 LOCUS AC021246 69570 bp DNA linear HTG 13-JUL-2000
PASFVVFLIQERVSKARHLQFISGVKPVIYWLSNFWDDKUNYVPATLVIIFICFQQ KSYVSSTNLPVLALLLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLPIGINGSVA IFVLEDFTONKLNNINDILKSYPELIFPHFCLGRGLIDWYKNQAADALERFGENREVS PLSWOLVGRNLPAMAVEGVVFFLITVLIQYRFPIRPPWARKLSPLNDEDEDVRRERQ RIEDGGCONDILEIKERLKIYERKRRAVDRICYGIPPOSCFGLLGVNGAGKSSFFRM ITGDTIVTRGDAFINKNSILSNIHEVHQNWGYCPQFDAITELLTGREHVEFFALLRGV PRESSYGKYGEMATRKLGFYKYGEKSYARKSGGRRKKISPAMALGOGPPVROLDEPTTG MOPKARRFLWNAALSVYKEGRSVVLTSGSMEEGCALCFGRAAIKVNGRFRCIGSVQHIX NRFGDGTIVVRAGSNPDLKPVQDFFGLAFGSVKKEKHRNMLQYQLPSSILSSLARI FSILSSSKRRHLMIEDYSVSQITLDQVFVNPRKQSSDDHLKDLEHKNGIVVDVAVLT	exon 7289372986 /gene="abcA1"	exon 7752077661 /gene="ABCA1"	exon 78931. 79049 /gene="ABCA1" /numbe=2	/gene="Ascala /gene="Ascala /number=6 1041520432	/gene="ABCA1" /number=7 exon 117287. 117379 /gene="ABCA1"	T=8 - 122569 - ABCA1" F=9	exon 125285125424 Qx /gente="ABCA1" Qx /mumbe=1.0 exon 125754125870 DE	11.7 50276 11.7	/ fumber=12 131023.13128 /gene"ABGA1" /number=13	31925 A1" 33330	86	/number=16 136959, .137163 /gene="ABCA1" /numbez=17	exon 13828. 138381 /qene="ASCA1" /number=18 exon 140179. 140350		12919	exon 143123143260 / Apple = "ABCAl" / number = 22 exon 143953144183 / gene = "ABCAl"

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(341: 940 of 100 bp 15196: contig of 655 bp in length 15196: contig of 655 bp in length 1623: contig of 827 bp in length 1702: contig of 849 bp in length 1702: contig of 849 bp in length 1804: contig of 869 bp in length 1804: contig of 869 bp in length 1909: gap of 100 bp 1909: gap of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5770: gap of 100 bp 100
                                                                                                                                                                    0476; gap of 100 by 1322; contig of 846 bp in length 12302; contig of 880 bp in length 13302; contig of 880 bp in length 13580; contig of 878 bp in length 1380; gap of 100 bp 14241; contig of 861 bp in length 14241; contig of 861 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1865: contig of 844 bp in length 2285: app of 100 bp 2285: app of 100 bp 2285: contig of 867 bp in length 332: gap of 100 bp 23780: contig of 848 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10: gap of 100 bp 32368: contig of 888 bp in length 68: gap of 100 bp 33312: contig of 844 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33313 33412: gap of 100 bp 33413 34268: contig of 856 bp in length 34269 34369: gap of 00 p 100 bp 35204: contig of 836 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66: gap of 100 bp 20921: contig of 855 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80: gap of 100 bp
24733: contig of 853 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55: gap of 100 bp 31410: contig of 855 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p of 100 bp contig of 852 bp in length
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872 bp in length
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38083: contig of 855 bp in length
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42824: contig of 811 bp in length
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contig of 875 bp in
                                       of 100 bp
contig of 851 bp
                                                                                                       of 100 bp
contig of 846 bp
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40967.
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25670: con
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                         9430: Com
                                                                                                           0: gap of
10376: con
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35305 3615
36157 36256:
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21966 2283
22833 22932:
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39032 39131:
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Bliren, B., Linton, L., Nusbaum, C., Lander, F., Abraham, H., Allen, N., Barra, N., Beckerly, R., Beddin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boguslavkiy, Collins, S., Collymore, A., Cocke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferrelra, P., FitzHugh, M., Forres, C., Gage, D., Galagan, J., Ferrelra, P., FitzHugh, M., Forres, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Liel, G., Locke, K., Macdonald, P., Marquis, N., Morban, P., McGurk, A., McKernan, K., McRentan, K., McRentan, K., Merchan, J., Meneus, L., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Pierre, N., Sautos, R., Severy, P., Spencer, B., Stange-Ihoman, N., Stojanovic, N., Subramanian, A., Talamas, J., Tasfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W., J., Marker, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced 91:6705871.
All repeats were identified using RepeatMasKer:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasKer.html
                                                                                                                                                                                                            Sukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Sutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 69570)
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sapiens clone RP11-1N10, LOW-PASS SEQUENCE SAMPLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOIE: This record contains 73 individual
* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
arbitrary. Low pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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1835 2804: contig of 870 bp in length
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Eukarycta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                        41349 TCCCCCCAACTCCCCTATA_GTGTCGTGGGGGGCTGAACGTCGCCCGTTAAGGGGGGGG 41408
                                                                   41469 GGCGGGGAGGAGGAGAGCACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCC 41528
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                                                                                                    378 GGCGGGGAGGAGGGAGGAAGCATTIGACCGATACTAACTCTCTGCGCTCGGTGCAGCC
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                                                        318 CCCCGGCTCCACCTGCTTTCTGCTGAGTGACTGAACTACATAAACAGAGGCCGGGAACGG
                                                                                                                                                GGCCGGGACCCGCAGACCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCCG
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Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S.
Regulatory nucleic acid sequences of the abol gene
Patent: Wo 0183746-A 3 08-NOV-2001;
Aventis Pharma S.A. (FR)
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7852 bp in length
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856 bp in length
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23: contig of 81

4083: gap of

61935: cr
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57163: contig of
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60020: contig of
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56197: contig of
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53328: contig of
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380: gap of 100...

14241: contig of 861 bp in 100 bp ...
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                                                                                                                                                                                                                                                                                             ACUZ1246 59570 bp DNA linear HTC 13-JUL-230C
Homo sapiens clone RP11-1N10, LOW-PASS SEQUENCE SAMPLING.
AC021246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 520 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6705871. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1897)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelecstomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 69570)
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                                        CATAAACAGAGGCCGGGAACGGGGGGGGGGAGGGAGGAGCACAGGCTTTGACCGATAGT 415
                      GICGCCCGTTTAAGGGGCGGCCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTA 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://itp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This record contains 73 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blinen,B., Linton,L., Nusbaum,C. and Lander,E.
Homo Sapiens chromosome, clone RPI1-1N10
Unpublished
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57163: cont.i
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48551: مما
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Saldwin, J., Barna, N., Beckerly, R., Beda, F., Boushgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Brown, A., Burkett, G., Castle, A., DeArellano, K., Dewar, K., Domino, K., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, K., Doyle, M., Fenestor, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Hagos, B., Heaford, A., Horton, L., Lahoczky, J., Levine, R., Jones, C., Zann, L., Karatas, A., Klein, J., Macdonald, P., Marquis, N., McEwan, P., McGhrk, A., McKernan, K., McPheters, R., Meldrim, J., Morbwan, P., Morbwan, Y., Maylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
                                                                                                    67642 CCCCCCNNCCCCACCACCACCACCANTNATAAGATGTCTCGTGGGGGGGGCACGTCGCC 67583
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                                                             CGTTTAAGGGGCGGGCCCCCGGCTCCACGTGCTTCTGCTGAGTGACTGAACTACATAAAC 362
                                                                                                                                                                                                                     GCGCTCGGTGCASCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCGTAATTGCG
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Smit, A.F.A. & Greer, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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   Indels
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Project Information

Length 69570;

48.2%;

in jn

100 bp of 907 bp

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1309: gap of 100 bp 12221: contiq of 912 bp in length 12321: gap of 100 bp 13205: gap of 100 bp 13205: gap of 100 bp 14325: gap of 100 bp 100 bp 14325: gap of 100 bp 100 
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37422: contig of 882 bp
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38402: contig of 880 bp
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                                                   * NOTE: This record contains 92 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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Pullinger.C.R., Hakamata,H., Duchateau,P.N., Eng.C.,
Aoulzerat,B.E., Fielding,C.J. and Kane,J.P.

Sibmitted (19-APR-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San
Prancisco, CA 94143-0130, USA
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Pullinger.C.R., Hakamata,H., Duchateau,P.N., Eng.C., Aouizerat,B.E., Fielding,C.J. and Kane,J.P. Analysis of FABCI gene 5' end: additional peptide sequence, promoter region, and four polymorphisms Biochem. Blophys, Res. Commun. 271 (2000) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                        87743 CCACTCCCCACTCATAGIGICTCGCCGCTGAACGICGNCCG-TTAAGGGGCGGGCCCC 87585
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                                                                                                                                                                                               40.7%; Score 229.8; DB 2; Length 90698; Similarity 66.0%; Pred. No. 9.7e-45; 9; Conservative 0; Mismatches 141; Indels 3;
               65976 66075: gap of 100 bp 66076 66954: contig of 879 bp in length 66076 66957: contig of 899 bp in length 67055 67947: contig of 893 bp in length 67948 68047: gap of 100 bp 68048 68934: contig of 887 bp in length 68035 69910: contig of 876 bp in length 69035 69910: contig of 876 bp in length 69911 70010: gap of 100 bp
65975: contig of 860 bp in length
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hes 279;
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/translation="wacwpolrllimknutprrrocolllevamplfffllisvrl
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198 c 190 g 156 t 1 others
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100.0%; Pred. No. 3.8e-31;
tive 0; Mismatches 0;
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1. .>697
                                                                                                                                                                                                  /note="membrane-bound"
Location/Qualifiers
1. .697
                                                                                                                                                                                                                                                                                                                   190 9
                                                                 /chromosome="9"
                                                                                                                                                                   396. .>697
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396. .>697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Vivology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalla; Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 736)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1532-3 Yana, Risarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
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AL514015
AG041031
CNS0072Q
BQ953024
AL554951
AG157500
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BQ944204
AG081217
CNSC10EW
CNS01720
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CNS00K3H
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Genomics Laboratory
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 Homo sapiens
Isogai, T.
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                                                                                    .; Search time 1057.18 Seconds (without alignments) 8559.210 Million cell updates/sec
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          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB; cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKPZ); Email s.wiemann@dkfz-heidelberg.de: sequenced by Qlagen (Hilden/Germany) within the CDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No sI sequence available.
This clone (DKFp5680N1210) is available at the RZPD in Berlin.
Please contact the RSZPD: Ressourcencentum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GFRMANY: Email: clone@rzpd.de.
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/clone_lib="686 (synonym: hlcc3)"
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/note="Vector: pM=18SFL3"
199 c 199 g 170
                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1002437"
/clone_lib="PLACE1"
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/lab_host="DH10B"
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EST (Duesterhoeft, et al.)
Unpublished (1999)
Contact: Duesterhoeft A
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Mammalia; Butheria; Primates: Catarrhini; Hominidae; Homo.
1 (bases 1 to 292)
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Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 70%)
Ota:T., Nishikawa;T., Suzuki;Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J.; Wakamatsu,A., Nakamura,Y., Nagai,I., Sugaro,S. and
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HRI human cDNA project; 5'- 6 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo. and
Helix Research Institute.
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
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Pred. No. 2.4e-10;
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/note="Vector: pME18SFL3"
205 c 260 g 158 t
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Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Dugrat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Altchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani Rabaktchis, C. and Tessier, A. IMAGE: molecular integration of the analysis of the human genome
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1 (bases 1 to 1004)
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Seq primer: (-21)M13_universal.
Location/Qualifiers
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1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
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Contact: MGC help desk
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Homo sapiens, clone IMAGE:4749735, mRNA.
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Tissue Procurement: James Cleaver, M.D.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genexpress@genethon.fr
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                                                                                                                                                                                                                                                                                                                                                                                    Tel: 33169472800
                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 33160778698
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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogasier BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINI at: http://image.llnl.gov series: IRAX Plate: 52 Row: d Column: 19 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5915657 This clone has the following problem: incomplete processing.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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S., Martin, R.G., Muzny, D.M.
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Eukaryota: Metazoa: Arthropoda; Hexapoda; Insecta: Pterygota;
Neoptera: Endopterygota: Diptera; Brachycera: Muscomorpha;
Ephydroidea: Drosophilae: Drosophila.
1 (bases i to 1201)
cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
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/do_xxefe"Hexoo:9606"
/do_xxefe"Hexoo:9606"
/clone="IMAGE:4749735"
/tissue_type="5kin, squamous cell carcinoma"
/clone_lib="NCI_CGAP_Skn4"
/lab_nos="BHIOSE" PRORY6.ccdb"
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Gunaratne, P. H., Garcia, A.M., Lu,
Yoon, V.S., Kowls, Car, Lawrence.
Richards, S., Gibbs, R.A.
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I (bases 1 to 998)
NIH-MGC http://mgc.rci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: James Cleaver, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The Lim.4.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution and be
                                                                                                                                                                                                                                                                       TGGTGCCCTTGGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGCGCAGCCCCGAGCCCAG 155
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                                                                                                                                     10.8%; Score 50.8; DB 17; 37.3%; Pred. No. 0.00055;
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/note="end: SP6"
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/db_xref="taxon:7227"
/clone="BACN15123"
                                   /clone_lib="DrosBAC"
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Submitted (12-AFR-2000)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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Roest-Crollius; H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F., Garnin, W. and Weissenbach, J. Brottler, P., Quetier, F., Firman gene number estimate provided by genome wide analysis using Tetraodon nigrouplished
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/organism="Terraodon nigroviridis"
/organism="Terraodon nigroviridis"
/db.xref="Texon:99883"
/close="115N17"
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Sost.Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fis
Bouncau, L., Biliault, A., Quetier, F., Saurin, W., Bernot, A.
Weissenbach, J.
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     Score 60.2; DB 12;
Pred. No. 0.00078;
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GSS; genome survey sequence.
Tetraodon nigroviridis.
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Web: www.genoscope.cns.fr.

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley proscopial Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs For further information please see http://www.fruitfly.org The BDGP Drosophila Adron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPGI 98 and was constructed by partial correct Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPGI 98 and was constructed by partial isogenic strain v2; or bw Sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be location Qualifiers

Location/Qualifiers

Location Value of Cancer Specifier Can be added to the BACPAC Resource Center Can be also the Condant at the World Cancer Cancer Cancer Center Can be also the Condant Cond
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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
221 AGACACCIGIACCCICCACCCCCACCCCACCCACCICCCCCAACICCCIAGAIGIG 280
                                   98 GIGCCCTICGCTGCCGGGAACGIGGACTAGACAGICTGCGGGCGCAGCCCGAGCCCAGCG 157
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Ephydroidea, Drosophilidae, Drosophila.
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/clone="BACR11P16"
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDCP). The BDCF is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDCP brosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Rowell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecost digestion of Prosophila DNA provided by the BDCP from the isogenic strain vis. or by, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order Individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be incoming the authorization display and the strain of the library of the library or filters for hybridization from the BACPAC Resource Center can be incoming at http://Dacepac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14J21 of RPCI-98 library from Drosophila melanogaster (fruit
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481 S----MYCCCMCSSMCCSWCSVCAVCSSGSVRSVAVGCSVGGRVGGSSRGRAGRS 535
                                                                                                                                                                                                              596 GGGSRVSSCSSGSSSSSSGCSGVSRSRRSGSANGVRVGGSGRRGGGGGRRGGANARAD 655
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Neoptera; Endopterygota: Diptera; Brachycera; Muscomorpha:
Ephydroidea: Drosophilidae; Drosophila.
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                                                                   278 GTGTCGTGGGCGGCIGAACGICGCCCGTTTAAGGGGGGGGCCCCGGCTCCACGTGCTTIC
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/clone="3ACR14J21"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC and Genevieve Payam. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 BVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                           CNSC15XC 832 bp DNA linear GSS 26-JUL-19
Drosophila melancgaster genome survey sequence T7 end of BAC
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha:
Ephydroidea; Drosophilidae; Erosophila.
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/db_xref="taxon:7227"
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RESULT 12

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Determination of this BAC-end sequence was carried out as part of collaboration of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs For further information please see http://www.fruitily.org The BDGP prosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the 'sogenic Strain y2: on bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://becpac.med.buffalo.edu/drosophila_bac.htm.
CUNSUUMLE GSS 03-JUN-1999
DIOSOPHILA Melanogaster genome survey sequence TET3 end of BAC #
BACREPOIG 66 RPOIL 98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endoptera; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton pBeloBACII.
                                                                                                                                                                                                                                                         Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
                                            Drosophila melanogaster genome survey sequence SP6 end of 3AC 19 BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL108450 GI:5628764
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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RESULT 14

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Prince that the Border of this Education with the Berkeley Drosophila Genome Project (EDGP). The EDGP is constructing a physical map of the Drosophila melanogaster genome using these Education of the Drosophila melanogaster genome using these Education of the Drosophila melanogaster Education was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jons's Laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The Library is anamed RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual Educ clones, the entire library or fillters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
CNSOO6EZ

CNSOO6EZ

Brosphila melanogaster genome survey sequence TET3 end of BAC #
BACKI18ELS of RPCI-98 library from Drosophila melanogaster (fruit
AL064271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref&genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASSGHGCSSCGSSGSGSGYSACCCMCCSCYCCCCSCYCYYCSCSCTCKTTTCGBGBSC 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIGGTGCCCTTGCCTGCCGGGAACGIGGACTAGAGAGICTGCGGCGCAGCCCGAGCCCA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          809 CSSGIGTICTSSSCTTTGCGCKSSSGGTSSSCBITBICGSCSTCSSSTCCTCSTTTCCG 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              749 GSCSTYSSSSTTCBKCSSSGSGSKANVKSGBSGGCSSYVVGSASMSSCGGKASAGKGRKS 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta, Pterygo
Neoptera, Badopterygota, Diptera; Brachycera, Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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Live 74; Mismatches 98; Indels 0
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/db_xref="taxon:7227"
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/clone_lib="RPCI-98"
/note="end : TET3"
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                                                                                                                                                             AL064271.1 GI:4944346
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Direct Submission
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- Web: www.genoscope.cns.france.to.mail: sequelegenoscope.cns.if.
- Web: www.genoscope.cns.france.to.mail: sequelegenoscope.cns.if.
Determination of this BAC-end sequence was carried out as part of collaboration with the Serkeley Drosophila genome project (BDGP).

The BJGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org.The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pater de Jong's Laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The Library is named RPCI-98 and was constructed by partial Ecoki digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and hotely individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://dagato.ned.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                    Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoplera; Endopterygota; Diptera; Srachycera; Muscomorpha;
Ephydroidea; Drosophila.
1 (bases 1 to 844)
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/db_xref="taxon:727"
/clone="BACR1P16"
/clone=11b="RPCI-98"
/note="end : TET3"
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17.8%; Pred. No. 0.
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Search completed: February 4, 2003, 03:26:21 Job time : 1080.9 secs

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DB 4; Length 595;
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                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Roizmen, Bernard
APPLICANT: Chou, Joany
TITLE OF INVENTION: Diseases
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTI SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
JS-09-235-103-1
                                                                                                                                                                                                                                                                                                            ALIGNMENTS
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RY: United States of America
60606-6402
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07-MAR-95
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Patent No. 6172347
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: DNA (genomic)
US-08-483-533-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 31-MAR-92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312/474-6300
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APPLICATION NUMBER: 08/
FILING DATE: 11-APR-95
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 595 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION:
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    TELEPHONE:
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Sequence 17, Appli
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Sequence 19,
Sequence 14,
                                                                                                      February 3, 2003, 12:56:40 ; Search time 26.4714 Seconds
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Seguence 38,
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Sequence 3,
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
               GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-283-471A-4
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US-09-483-471A-36
PCT-US91-06532-1
US-09-041-886-18
US-08-018-977C-4
US-08-018-977C-4
US-08-072-574-7
US-08-061-375-4
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US-09-073-840A-1
US-09-103-840A-1
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US-08-483-533-38
US-09-283-471A-38
US-07-841-646-3
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                               Score 38.8: DB 4; Length 595; Pred. No. 0.083; 0; Mismatches 132; Indels
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South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Method for Treating Tumorigenic TITLE OF INVENTION: Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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COUNTRY: United States of America
ZIP: 60606-6402
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07-MAR-95
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Sequence 36, Application US/08483533
Patent No. 6172047
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6300 Sears Tower, 233
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Roizman, Bennard
APPLICANT: Chou, Joany
                                   6.98;
                                                   49.2%;
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nucleic acid
EDNESS: single
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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                                                                  Matches 131; Conservative
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APPLICATION NUMBER: (
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
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APPLICATION NUMBER:
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                                 Query Match
Best Local Similarity
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US-09-283-471A-4
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                                                 92 CCACTGGTGCCCTTGGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGCGCGAGCCCCGAGC 151
                                                                                                                     Gaps
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APPLICANT: Chou, Joany
TITLE OF INVENTION: Method For Treating Tumorigenic Diseases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall ...
                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2: Marshall, O'Toole, Gerstein, Murray & 6300 Sears Tower, 233 South Wacker Drive
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                0; Mismatches 132;
Pred. No. 0.083;
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COUNTRY: United States of America
ZIP: 60605-6402
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09283471A Patent No. 6340673 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/661,233
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
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MOLECULE TYPE: DNA (genomic)
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/48
49.28;
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nucleic acid
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TELEPHONE: 312/474-6448
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                Conservative
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity
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STREET: bov.
TTW: Chicago
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APPLICANT:
            Matches 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36, Application US/09283471A
Patent No. 6340673
GENERAL INFORMATION:
APPLICANT: Rolzman, Bernard
APPLICANT: Chor, Joany
TITLE OF INVENTION: Method For Treating Tumorigenic Diseases
                                                      Length 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/283,471A FILING DATE: 04 APR-1999 CLASSIFICATION: 514
                                                Query Match
6.9%; Score 38.8; DB 4;
Best Local Similarity 49.2%; Fred. No. 0.11;
Matches 131; Conservative C; Mismatches 132;
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COUNTRY: United States of America
ZIP: 60606-6402
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31-MAR-1992
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 11-APR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILLING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Zeller, James P. REGISTRATION NUMBER: 2
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APPLICATION NUMBER: 0
FILING DATE: 11-APR-1
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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TTTY: Chicago
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US-08-483-533-36
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                                                      Query Match
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92 CCACTGGTGCCCTTGGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGCGCAGCCCGAGC 151
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                                                                                                                Length 1327;
                                                                                                                                                       0; Mismatches 132; Indels
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TITLS OF INVENTION: Recombinant Herpes Simplex Viruses
TITLE OF INVENTION: Vaccines and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/06532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Bicknell
                                                                                                              Score 38.8; DB 4;
Pred. No. 0.11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 CGTGCTTTCTGCTGAGTGACTGAACT 354
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                                                       MOLECULE TYPE: DNA (genomic) US-09-283-471A-36
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                                                                                                                Query Match 6.9%;
Best Local Similarity 49.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 36,0
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                       Matches 131; Conservative
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DEDNESS: single
IYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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TOPOLOGY: 111
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PCT-US91-06532-1
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PCT-US91-06532-1
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133 CTGCGGCGCAGCCCCGAGCCCAGCGTTCCCGCGGTCTTAGGCCGGCGGGGCCGGGCCGG
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                                 108 CIGCCGGGAACGIGGACTAGAGAGICIGCGGCGCAGCCCCGAGCCCAGCGCTICCCGCGC 167
                                                                                                                                                  168 GTCTTAGGCCGGGGGCCCGGGGGGAAGGGGAACGCAGACCGCGGACCCCTAAGACACC
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TITLE OF INVENTION: DNA Sequences Encoding Mutant Antiviral
TITLE OF INVENTION: Regulatory Proteins
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MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb storage
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ADDRESSEE: The Pennsylvania State University
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APPLICATION NUMBER: US/08/018,977C
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APPLICATION NUMBER: 07/726,071
FILING DATE: 05-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-018-977C-4/c
; Sequence 4, Application US/08018977C
; Patent No. 5686601
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CITY: University Park
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OPERATING SYSTEM: MS-DOS 6.22
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TELECOMMUNICATION INFORMATION:
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TELEFAX: (814) 865-3591
INFORMATION FOR SEQ ID NO: 4:
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es 76; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                   92 CCACTGGTGCCCTTGGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGGCGCAGCCCCGAGC 151
                                                                                                                                                                              3; Gaps
                                                                                                                                                                                                                                                                                                                                                            CSGACCCTAAGACACCTGCTGTACCTCCACCCCACCC - - - CACCCACCTCCCCCAAC
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Score 38 8; DB 5; Length 1335; Pred. No. 0.11; 0; Mismatches 132; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bradesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryr A.
REGISTRATION WUMBER: 31,915
REFERENCE/DCCKET UNMBER: 9-LJ 2626
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 CGTGCTTTCTGCTGAGTGACTGAACT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  788 egeccedeageegeccaacceger 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/09041885
Patent No. 6235872
GENERAL INFORMATION:
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
         6.98;
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                                                                   Conservative
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STREET: 43/0_CITY: San Diego
TIX: Callfornia
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SOFTWARE: Patentr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
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                                                                Matches 131;
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18478 GCCACGCGTCGCGGGCACCGCCGAGCTCGCACTCCGCGACGGCACC 18526

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ZIP: 0C719
COMPOTER REACASLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPOTER: PBM PC COMPOTER:
COMPOTER: PC-DOS/MS-DOS
RESULT 9
US-08-072-574-7/c
Sequence 7, Application US/08072574
; Patent No. 5521297
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGIGSRATION NUMBER: 31,192
REBERNCE/DOCKET NUMBER: P41
TELEPHONE: 213-622-7700
TELEPHONE: 213-489-4210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4085 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, S
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STRANDEDNESS: both
                                                                                                                                                                                                                        STREET: 444 COUNTY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       both
                                                              GENERAL INFORMATION: APPLICANT: Dagget
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                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                             STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                              APPLICANT: Desoff, Sradley S.
APPLICANT: Kulstoss, Stiart A.
APPLICANT: Kosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36.2; DE
Pred. No. 2.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             US/08/804,227C
                                                                                                                                                                             SEE: THOMAS G. FLANT 1501
: LILLY CORPORATE CENTER
INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-8231
             Sequence 1, Application US/U8804227C Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: Defoff, Stadley S.
                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCI(DOS) TEXT ONLY CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804
FILING DATE: February 2-, 1999
FLING DATE: Rebruary 2-, 1999
FLASSIFICATION: 435
ATORNERS/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
                                                                                                                                                                                                                                                                                                                                                Text only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEPERENCE/DOCKET NUMBER: X-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 50.9%;
Matches 86; Conservative (
                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 43280 base pairs
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14351..19945
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20010..31199
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31232..36067
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36249..41774
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LOCATION:
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LOCATION:
                                                                                                                                                                                  ADDRESSEE:
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   JS-08-804-227C-3
                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                SIREET:
CITY: IN
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3273 CACCECCTTGGGGCCGGCGTCTGGCGACTCGGGCCGCCTGGGCCGCGCGCCTGCGCAGCC 3214
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APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen
APPLICANT: Pontsler, Aaron
TITLE OF INVENTION: BUNGAN MATABOTROPIC GLUTAMATE RECEPTORS.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
6.3%; Score 35.8; DB 1; Length 4085;
Best Local Similarity 50.3%; Pred. No. 1.2;
Matches 88; Conservative 0; Mismatches 87; Indels 0
                                                                                                                                                                                                                       3: Pretty, Schroeder, Brueggemann & Clark
444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NAMSER: US/08/072,574
FILING DATE: 19930604
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . OTHER INFORMATION: /product= "HUMAN MGLUR5A" US-08-072-574-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-08-072-574-9/c
; Sequence 9, Application US/08072574
; Patent No. 5521297
; GENERAL INFORMATION:
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NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE:
US-08-061-376-4
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                                                                                                                                90071
                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-103-840A-1
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US-09-103-840A-1
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                                                                                            STATE: C
                                                      STREET:
CITY: L
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APPLICANT: Diabali, Malek
APPLICANT: Diabali, Malek
APPLICANT: Selleri, Licia
APPLICANT: Selleri, Patline
TITLE OF INVENTION: CHARACTERIZATION OF A CHROMOSOME 11Q23
TITLE OF INVENTION: TRANSLOCATION BREAKPOINT ASSOCIATED WITH ACUTE LEUKEMIAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "HUMAN MGLUR5B"
/note= "variant of MGLUR5A with 96 base pair
insertion between nucleotides 2999 and 3000."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 CCCCCAACTCCCTAGAIGTGTGTGGGGGGGCTGAACGTCGCCCTTTAAGGGGCG 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4181;
                                                          APPLICANT: Pontsler, Aaron
TITLE OF INVENTION: HOMAN MATABOTROPIC GLUIAMATE RECEPTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES TH
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87; Indels
                                                                                                                                                      E: Pretty, Schroeder, Brueggemann & Clark
444 South Flower Street, Suite 2003
                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB î;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.3%; Score 35.8; Di
Best Local Similarity 50.3%; Pred. No. 1.2;
Matches 88; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/072,574
FILING DATE: 19930604
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                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Reiter, Stephen E. REGISTRATION NUMBER: 31,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-622-7760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 213-489-4210
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4181 base pairs
      Daggett, Lorrie
Ellis, Steven B.
Liaw, Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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LOCATION: 370..4008
OTHER INFORMATION: /
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EDNESS: both
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OTHER INFORMATION:
                                                                                                                                                        ADDRESSE: Pretty,
STREET: 444 South
CITY: Los Angeles
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US-08-061-376-4/c
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                        APPLICANT:
APPLICANT:
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        APPLICANT:
                                                                                                                                                                                                                                COUNTRY:
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196 AAGGGGACGCAGACCGCGGACCCTAAGACACCTGCTGTACCCTCCACCCCACCCCACCCC 255
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APPLICANT: WHITE, Owen R.
APPLICANT: FLEISCHMAN, ROBERT M.
APPLICANT: PRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM FILE REFERENCE: 24366-20007.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 GGGAAGCAGGGCCGGGACGCTTGCGCTGGGCCCCCTAGGCCCGGGGCCCCCC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.3%; Score 35.8; DB 4; Length 11907; 50.9%; Pred. No. 1.8; 1.00 Mismatches 82; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 ACCICCCCCAACICCCIAGAIGIGICGIGGGGGGGGTGAACGICGCC 302
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SSEE: Pretty, Schroeder, Brueggemann & Clark
: 444 South Flower Street, Suite 2000
California
                                                                                                                                                                                                                                                        OPERATING SYSIEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.6, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/061,376
FILING DATE: 13-MAY-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/0910384CA Patent No. 6294328 GENERAL INFORMATION:
                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,192
REPERENCE/COCKET UNMBER: P4,
TELECOMMUNICATION INFORMATION:
TELEBHONE: (619)546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 11907 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 13-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Reiter, Stepher 3 REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (619)546-9392
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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TELEFAX:
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APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
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APPLICANT: WHILE, OWER R.
APPLICANT: WHILE, OWER R.
APPLICANT: WHILE, OWER R.
APPLICANT: VENTER, John C.
TILLE OF INVENTION! DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCCBACTERIUM
TILLE OF INVENTION: TUBERCOLOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NOWBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
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                                            0; Gaps
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55.7%; Pred. No. 17;
tive 0; Mismatches 54; Indels 0;
Query Match 6.3%, Score 35.6; DB 4; Length 4411529; Best Local Similarity 54.2%; Pred. No. 17; Matches 77; Conservative 0; Mismatches 65; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Seidel, Gonda, Lavorgna & Monaco, P.C. STREET: Two Penn Center, Suite 1800 CITY: Philadelphia CITY: Pennsylvania COUNTRY: 11 country:
                                                                                                                                                                                                                                                                                                                     Db 1630791 GGCCACCGGTCCCACCGGTGCC 1630812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/08306691B Patent No. 5734039 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             261 CCCCCAACTCCCTAGATGTGTC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 55.73
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-08-306-691B-19/c
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Db 836329 CC 836328
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APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 CTAAGACACCTGCTGTACCCTCCACCCCCACCCCACCTCCCCCCAACTCCCTAGAT 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 GIGTCGTCGCCGCCTGAACCTCGCCCGTTTAAGGGGCGGGCCCCGGCTCCACGIGC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 35100;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza
COMPUTER READABLE FORM:
NDELUM TYPE: Diskette, 3.50 inch, 720 KD COMPUTER: IBM PS/2COMPUTER: IBM NS-DOS COMPUTER: MOLGPERIECT 5.1
SOUTHWARE: WOLGPERIECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Pred. No. 4:
                                                                                                                                                                  APPLICATION NUMBER: US/08/305,691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application PC/TUS9306251 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin: Release 11.
SOFTWARE: Patentin: Release 11.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/C
FILING DATE: 19930630
CLASSIFICATION:
ATTORNEY-AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                    30,480
                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 83. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: NO. 5734039e
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                 : (215) 568-8383
(215) 558-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 35100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                        ACTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 400 Garden
CITY: Garden City
STATE: NY
COUTER: USA
ZIP: 11530
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Best Local Similarity
                                                                                                                                                                                                                CLASSIFICATION:
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US-08-306-691B-19
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REFERENCE/DOCKET NUMBER: 9586
TELECOMMUNICATION INFORMATION:
TELEPAN: 516-742-4364
TELETAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR ESQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 355.00 base pairs
TYPE: nucleic acid
STRANDENDESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-19
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0; Query Match 6.2%; Score 35.2; DB 5; Length 35100; Best Local Similarity 50.0%; Pred. No. 4; Matches 88; Conservative 0; Mismatches 88; Indels 0;

218 CTAAGACACCIGCTGTACCCTCCACCCCCACCCACCICCCCCCAACTCCCTAGAT 277

QQ

QY

δŏ ad Ωÿ Search completed: February 3, 2003, 18:51:27 Job time : 8913.47 Secs

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Porsch-Ozcurumaz,M., Langmann,T., Heimerl,S., Borsukova,H., Kaminski,W.E., Drobnik,W., Honer,C., Schumacher,C. and Schmitz,G.
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The zinc finger protein 202 (ZNF202) is a transcriptional repressor of ATP binding cassette transporter A1 (ABCA1) and ABCG1 gene expression and a modulator of cellular lipid efflux J. Biol. Chem. 276 (15), 12427-12433 (2001)
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                                                                                                                                      Submitted (05-0AM-2000) Porsch-Oezcueruemez M.K., Institute for Clinical Chemistry, Universitiy of Regensburg, Franz-Josef-Strauss-Allee II, 93042 Regensburg, GERKANY Location/Qualifiers 1.167
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/gene="ABC-1"
/function="cholesterol efflux regulatory protein"
/function="cholesterol efflux regulatory protein"
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                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
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/cell_:ype="leukocyte"
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Porsch-Oezcueruemez,M.K.
Direct Submission
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PAT 22-JAN-2001

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Mammalla, Eutheria: Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1643)
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1 (asses 1 to 1643)
Lawn, R.M., Wade, D. and Garvin, M.
Regulation with binding cassette transporter protein abcl
Patent: WO 0078972-A 3 28-DEC-2000;
CV TERRAPEUTICS, INC. (US)
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Atp binding cassette transporter protein abol polypeptides
Fatent: WO 0078971-A 3 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
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Human DNA sequence from clone RP11-217B7 on chromosome 9, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 96717)
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assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw.:, SWISSPROT: Tr., TREMEL: WO: WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMPORTANT: This sequence is not the entire insert of clone RP11-217B7 It may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true right end of clone RP11-217B7 is at 96717 in this sequence. The true left end of clone RP11-122R10 is at 72980 in this sequence. The true right end of clone RP11-3127B10 is at 2000 in
                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGSYChr9
RPP1-21787 is from the library RPCZ-11.1 constructed by the group of Pleter de Jong. Por further details see
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3238. .3778
Anote="Sequence from AF275948 sequenced by National
Institutes of Heath, National Heart, Lung and Blood
Institute, Bethesda, MD 20892, USA."
one plasmid subclone or more than one M13 subclose; and the
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/note="Sequence from overlapping clone RPI1-122F10
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                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.chori.org/bacgac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Romo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
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100 bp f 1531 bp in length

100 bp f 1994 bp in length

100 bp f 1270 bp in lengch

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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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76888: contig of 5330 bp in length
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f 1681 bp in length
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of 1707 bp in length
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17: contig of 3020 bp in length
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contig of 3054 bp in length
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28184: contig of 2377 bp in
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                                                                                                                                                                                                                                                           ACC1223C 175064 bp DNA linear HTG 22-APR-2000 Homo sapiens cione RPI1-1M10, WORKING DRAFT SEQUENCE, 39 uncrdered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (21-007-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 22, 2000 this sequence version replaced gi:6454933.
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia: Eutheria, Primates, Catarrhini, Eominidae, Eomo.
                                                              17269 GGCAAAAACCCCGTAATTGCGAGGGAGAGTGGGGCCGGGACCGGGAGAGCCGAGAGCCTAGCC 17210
  17329 CITIGACCGATAGTAACCICIGCGCTCGGIGCAGCCGAATCIATAAAAGGAACIAGICC 17270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                           GGCAAAAACCCCCTAATTGCGAGCGAGGTGAGTGGGGCCGGGACCCGCAGAGCCGAGGC 420
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator 31g Dye; 100% of reads Assembly program: Phrap; version 0.960731 consensus quality: 117571 bases at least Q40 consensus quality: 145749 bases at least Q30 Consensus quality: 146749 bases at least O30 Consensus quality: 160940 bases at least O30
                                                                                                                                           Birren, B., Linton, L., Nusbaum, C. and Lander, B. Homo, sapiens, clone RP11-1M10
                                                                                                                        GACCCTTCTCTCCCGGGCTGCGGCAGGCCAGGCGGGGAGCTC 463
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Insert size: 171264, sum-of-contigs
Quality coverage: 2.9 in 020 bases;
Quality coverage: 3.2 in 020 bases;
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Web site: http://www-seq.wi.mit.edu
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Center project name: L2510
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Homo sapiens.
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AC012230.3 GI:7637254
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AC012230
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100 bp 100 bp

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Manufard's Lucieria's Filmates's Cataffinish Hominidae's Homo.

(S Pulinger C.R., Hakamata, H., Duchateau, P.N., Eng.C.,
Abularath, E., Flediding, C.J. and Kane, J.P.
Abularath, E., Flediding, C.J. and Kane, J.P.
Abularath, E., Flediding, C.J. and Kane, J.P.
Biochem Biophys Res. Commun. 271 (2000) In press
(C Pases 224 to 1167)
Pulinger C.R., Hakamata, H., Duchateau, P.N., Eng.C.,
Abularath, E., Fleding, C.J. and Kane, J.P.

Submitted (20 Apr.-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San Francisco, CA 94143-0130, USA
3 (bases 1 to 1167)
Abularath, B.E., Fleding, C.J. and Kane, J.N., Eng.C.,
Abularath, B.E., Flediding, C.J. and Kane, J.P.
Direct Submission

Elakamata, H., Duchateau, P.N., Eng.C.,
Abularath, B.E., Flediding, C.J. and Kane, J.P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                       121 GACACCIGCTGLACCCTCCACCCCCCCCCCCCCCCCCCCCCCAACTCCCTAGATGTGT
                                                                                                                                                                                                              181 CGTGGGCGGCTGAACGTCGCCCGTTTAAGGGGCGGGCCCCGGGCTCCACGTGCTTTCTGCT
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On Jun 23, 2000 this sequence version replaced gi:7769713
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/db_xref="taxon:9606"
/chromosome="9"
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                     18160 145491: contig of 7332 bp in length 100 bp 10
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4516. 5785
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5886. 7879
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7980. 9686
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/note="assembly_fragment"
20232. .22587
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/note="assembly_fragment"
52719. .56592 /
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25808. .28184
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31439. .34299
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38419, 42835
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/note="assembly_fragment"
42936. .45448
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48217. .52618
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63762. .68437
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2735. .4415
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12354. .15228
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45549. .48116
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/note="assembiy_fragment
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/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 69570)
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Homo sapiens clone RPll-1N10, LOW-PASS SEQUENCE SAMPLING
AC021246
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224. .844
/gene="ABCA1"
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/gene="ABCA1"
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Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stoffanovian, N., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, E., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A., and Zody, M.
                                                                                                                                                                                                                                           Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                        for
                                                                                                    Direct Submission
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 13, 2000 this sequence version replaced gi:6703871. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
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7609: gap of 100 bp
8479: contig of 870 bp in length
579: gap of 100 bp
579: gap of 100 bp
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10376: contig of 845 bp in length
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15196: contig of 855 bp in length
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50441 50540; gap of 100 bp in length 50541 51404: contig of 864 bp in length 51405 51504 aga of 100 bp 52373: contig of 868 bp in length 52373 52472: gap of 100 bp 52473 52472: gap of 100 bp 53429 54568: contig of 856 bp in length 53429 54568: contig of 840 bp in length 54269 54366: gap of 100 bp
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46643: contig of 819 bp in length
46743: gap of 100 bp
47599: contig of 856 bp in length
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28: contig of 872 bp in length
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83: contig of 855 bp in length
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PAT 21-MAR-2001
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Pred. No. 4.8e-91;
0; Mismatches 2
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Sequence 1 from Patent WOOI15676.
AX092589
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               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalla, Eutheriay Primates, Catarrhini, Hominidae, Homo. (Dases 1 to 18399)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                           Hayden M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M. Compositions and methods for modulating hel cholesterol and triglyceride levels
Patent: WO 0115676-A 1 08-MAR-2001;
University of British Columbia (CA); Xenon Genetics Inc. (CA)
Location/Qualifiers
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                                                                                                                                                                                                                                                                Score 447; DB 6;
Pred. No. 1.1e-90;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 37944 c 41170 g 54950 t
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AX351029
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                                                                                                                                                                                                                                                                96.5%;
98.7%;
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Homo sapiens
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PRI 17-JUL-2000
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(Dases I to 149034)
Santamarina-Fojo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L.,
Cheng,J.F., Csorio,J., Remaley,A., Yang,X.P., Haudenschild,C.,
Praces,C., Chimini,G., Blackmos,E., Francois,T., Duverger,N.,
Rubin,E.M., Rosier,M., Denefie,P., Fredrickson,D.S. and Brewer,H.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete genomic secuence of the human ABCAI gene: analysis of the human and mouse ATP-binding cassette A promoter Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7887-7992 (2000) 20345099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                   Santamarina-Fojo.S., Peterson, K.M., Knapper, C.L., Freeman, L.A., Remaley, A.T., Yang, X.-P., Haudenschild, C.C., Blackmon, E.E., Francois, T.L. and Brewer, H.B. Jr.

Direct Submission
Submitted (08-JUN-2000) Molecular Disease Branch, National Institutes of Eacth, Rational Reart, Lung and Blood Institute, Bethesda. MD 20892, USA
Location/Qualifiers
                                                                                                                                                                                                       2517 CCTTGGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGCGCAGCCCGAGCCCAGCGCTTC 2576
                                                                                                                                                                                                                                                              2637 GACACCTGCTGTACCCTCCACCCCACCCCACCCCACCTCCCCCAACTCCCTAGA 2695
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                                                                                                                                 Gaps
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                                                                                             Length 3231;
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                                                                                             03 6;
                                                                                          Score 446.4; DB 6;
Pred. No. 2.3e-90;
0; Mismatches 1;
                                     773
/organism="Homo sapiens"
/db_xref="taxon:9606"
773 c 875 g 773
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98.78;
                                                                                                                               Conservative
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Best Local Similarity
Matches 462; Conserv
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| John (1654 | 1674,25831 | 125989,40385 | 40478,45012 | 145153, 46423 | 46511,6729 | 67850,70831 | 71007 83960 | 84052, 89000 | 89250,91962 | 92101,92431 | 925649,96758 | 96955, 97002 | 93950,91962 | 92101,92433 | 925649,96758 | 96955, 97002 | 93950,98062 | 926043 | 925649,96758 | 96955, 97002 | 93642 | 93664,100391 | 100615,102362 | 96955, 97002 | 93645 | 93664,100862 | 93664,100862 | 93664,102862 | 93664,10866 | 93664,10866 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664 | 93664
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/gene="ABCA1"

    149034
    crganism="Homo sapiens"
    db_xref="taxon:9606"

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/db_xref="GI:9247086"
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/rpt_family="Alt"
4240. 4509
/rpt_family="Alt"
4998. 5270
/rpt_family="Alt"
5563. 5839
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6615. :6877
/rpt_family="Alu"
8800. :9046
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15220. .15399
/rpt_family="Alu"
15508. .15787
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9998. .10279
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11859. 12133
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12810. .12902
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!8600. .18860
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20950. .21206
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25038. .2531
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CONTRACTOR TO THE TOTAL DILQDLIGRNISDYLVKTYVQIIAKSIÄNKIWVNEFRYGGFSLGVSNTQALPPSQEVN DAXKQMKKHLKLAKDSSADRFLNSLGREMTGLDTRNNVKVWFNNKGWEAISSFLNVIN PALIFANLOGRGENPSHYGITARNHPLNKTRQDLSDVAKMTSYDYLVSTCYIFAMSFV PASTVYFLLOGRGYSKAKHLQFISGVRYIYNLSNFWDMCNYVYPATLVIIFTCRQO KSYVSSINLPYLALLLLYGKSITPLMYPASTYFKIFDTAYVYLSTNHIFTGINGSVA TFVLELFIDNKLNNINDILKSVFLIFPHFCLGRGLIDMYKNQAMADALERFGENRFVS ARLFSDARRLLLYSQKDTSMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYH NLSLPKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELGGLP RQVMAEVNKTFQELAVFHDLEGMWEELSPKIMTFMENSQEMDLVRMLLDSRDNDHFWE QQLDGLDWTAQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNQAIRTISRFMECVNLN LTGDTTVTRGDAFINXNSLLSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGV PEKEVGKVGEWAIRKLGLVKYGEKYAGNYSGGNKRKLSTAMALIGGPPVVFLDEPITG MDPKARRFLMNCALSVVKEGRSVVLTSHSMEECEALCTRMAIMYNGRFRCLGSVQHLK NRFGDGYTIVVRIAGSNPDLKPVQDFPGLAFPGSVXKEKHRNMLQYQLPSSLSSLARI FSILSQSKKRLHIEDYSVSQ?TLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLT SWSDMRQEVMFLINVNSSSSSTQIYQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALF GGNGTEEDAETFYDNSTTPYCNDLMKNLESSPLSRIIWKALKPLLVGKILYTPDTPAT NKIKDGYWDDGPRADPFEDMRYVWGGFAYLQDVVEQAIIRVLTGTEKKTGVYMQMPY PCYVDDIFLRVWSRSMPLFWTLAMIYSVAVIIKGIVYEKEARLKETMRIMGLDNSILW FSWFISSLIPLLVSAGLLVVILKLGNDLPYSDPSVVFVFLSVFAVVTILQCFLISTLF SRANLAAAGGGIIYFTLYLPYVLCVAWQDYVGFTLKIFAXLLSPVAFGFGCEYFALFE PLSWDLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQ RILDGGGQNDILEIKELTKIYRRKRKPAVDRICVGIPPGECFGLLGVNGAGKSSTFKM KLEPIATEVWLINKSMELLDERKFWAGIVFIGITPGSIELPHYKYKIRMDIDNVERT SFLQDEKVKESYV"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1377 ACAGGCTTTGACCGAZAGTAACCTCTGCGCTGCAGCCGGAATCTATAAAAGGAACTA 1436
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 149034;
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ORGANISM
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Qiu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
Scanfitted (13-301-2000) Genome Science Department, Lawrence
Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,
CA 94720, USA
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Qiu,Y., Cavelier,L., Chiu,S., Yang,X., Rubin,E. and Cheng,J.F. Human and mouse ABCAL comparative sequencing and transgenesis studies revealing novel regulatory sequences Genomics 73 (1), 66-76 (2001)
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141340. .14
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143123. .14
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Elizen, B. (Jases 1 to by 2)()

Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Allen, N., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Cocke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Mardus, J., Erthugn, M., Porrest, C., Gage, D., Galagan, J., Ianders, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McChar, J., Narjor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Piterze, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Strojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (16-Jan-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA C2141, USA

All repeats were identified using RepeatMasker:

Sait, A.F. A. & Green, P. (1996-1997)
Http://Tp.genome.washington.edu/RM/RepeatMasker:html
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                           Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * sequencing reads that have not been assembled into * contigs. But sof N are used to separate the reads * and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for * identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. * Howerr, it should not be assumed that this clone * will be sequenced to completion. In the event that the record is updated, the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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100 bp
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                                                                                                                Mammalia; Eutheria: Primates; Catarrhin; Homil (bases 1 to 69570)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This record contains 73 individual
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Center clone name: 1_N_10
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6540: con
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  GI:9119882
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HIG; ETGS_PEASE0.
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                                                                                                                                                                              AUTHORS
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AC021246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                33854 ACAGGCTTTGACCGATAGIAACCTCTGCGCTGCAGCCGAATCTATAAAAGGAACTA 33913
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                                                        76.8%; Score 355.4; DB 6; Length 2893; larity 98.4%; Pred. No. 6.6e-70; Conservative 0; Mismatches 1; Indels 5;
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/db_xref="taxon:9606"
1 681 c 769 g 698
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Query Match

Matches

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LOCUS DEFINITION ACCESSION RESULT 13 AC021246/c

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16224 17072: contig of 849 bp in length 17073 17172: gap of 100 bp 17173 15041: contig of 859 bp in length 18042 18141: gap of 100 bp 18042 18141: gap of 100 bp 18042 18142 19009: contic of efficient
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39031: contig of 848 bp in length
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contig of 836 bp in length
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21: gap of 100 bp
21865: contig of 844 bp in length
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837 bp in length
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827 bp in length
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21: contig of 851 bp in
gap of 100 bp
76: contig of 855 bp in
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contig of 855 bp In
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878 bp
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contig of 980 bp
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25670: contig of
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13280: contig of
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16123: conf
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19966: cont
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33447: contig of 895 bp in length

347: gap of 100 bp

3435: contig of 888 bp in length

535: gap of 100 bp

55433: contig of 898 bp in length
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                                                                                                                                                                                                                                                                           MCU21345 90698 bp DNA linear HTG 13-JUL-2000
HOMO sapiens clone RP11-2449, LOW-PASS SEQUENCE SAMPLING.
AC021345
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Submitted (16-3A)-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
on Jul 13, 2000 this sequence version replaced g1:6705761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata, Craniata, Vertebrata, Euteleostomi, Primates, Catarrhini, Hominidae, Homo.
------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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101 1010: gap of 100 bp
101 1873: contig of 863 bp in length
1874 1973: gap of 100 bp
1974 2824: contig of 851 bp in length
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                                                                                                                         67342 GACAGGACAGGCGGGAGCTC 67321
                                                                                            442 GGCAGGCCAGGCGGGAGCTC 463
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HTG; HTGS_PHASE0.
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Mammalia, Butheria, Pr
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COMMENT

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Query Match

Query Match

Best Local Similarity 66.0%; Pred. No. 7.8e-42;

Matches 279; Conservative 0; Mismatches 141; Indels 3; Gaps 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (19-APR-2000) Cardiovascular Research Institute, University of California, San Francisco. 505 Parnassus Avenue, Francisco CA 94143-0130, USA iocation/Qualifiers
                                                                                                                                                                               GGGAGGAGGAGACACCACGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAAT 340
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Best Local Similarity 100.0%; Pred. No. 7.7e-29;
Matches 173; Conservative 0; Mismatches 0; Indels 156 ± 190 g 198 c 152 a BASE COUNT ORIGIN

Op ŏŏ QQ

Q7 Db

Search completed: February 4, 2003, 01:26:54 Job time : 1675.59 secs

Title: Perfect score:

Sequence

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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AL309889 Tetracdon
AL066742 Drosophil
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BQ680479 AGENCOURT
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Mammalla; Butherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 736)
Ota/T., Nishikawa/T., Suzuki,Y., Ishili,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Fax: 81-438-52-3086
Email: genomics@hri.co.jp
EMRI buman CDNA project: 5'- a 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Genomics Laboratory
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                                                                                                 February 3, 2003, 16:39:45 ; Search time 875.075 Seconds
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              GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compuges Ltd.
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/db_xref="taxon:9606"
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Contact: Takao Isogai
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DKF2p686N12109_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKF2b686N12109 5', mRNA sequence.
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Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 547)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No sI sequence available.
This clone (DKRZp586M12109) is available at the RZPD in Berlin. Please contact the RZPD. Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GFRMANY: Email: clone@rzpd.ce.
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/dev_stage="adult"
/lab_host="DH10B"
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/tissue_type="placenta"
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/clone="DKF2p686N12109"
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Socation/Qualifiers
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Unpublished (1995)
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AL698654
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Separate.

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292 bp mRNA linear BST 14-NOV-1994 HSC12B081 normalized infant brain cDNA Homo sapiens cDNA clone c-12b08, mRNA sequence.
                       EST 01-AUG-2002
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Marmalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 292)
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordara; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 763)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kiarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3966
Email: genomics@hti.co.jp
HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix
Research Institute: cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                            Ota'T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375 AATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCC 434
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/note="vector: pME18SFL3"
205 c 260 g 158 t
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Homo sapiens
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/dev_stage="3 months old"
/dev_stage="3 months old"
/note="corpan: brain: Vector: lafmid BA: Site_1: HindIII;
Site_2: NotI: sex=Female: dev_stage=3 months old;
isolate=muscular arrophy patient: tissue_type=total brain
cotal mRNA was oligo-(dT) primed and directionally
cloned 5: > 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA: Normalization_method:
Bento Soares, P.N.A.S in press"
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Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes 'M.D., Dugrat, S., Goulgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani-Kabaktchis, C. and Tessier, A. IMAGE: molecular integration of the analysis of the human genome
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (24-JUL-2002) Mational Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Gencmics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    389 GIGAGIGGGGCCGGGACCCGCAGAGCCGACCCTTCTCTCTCCGGGGTGCGGCAGGG 448
                                                                                                                                                                                                                                                                                                                                  Genexpress_library_idt: C, Genexpress_sequence_idt: y_c-1zb08
Seq primer: (-21)M13_universal.
Location/Qualifiers
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Genethon Centre de recherche sur le Gesome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
                                                                                                                            Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="normalized infant brain cDNA"
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3.3e-08;
hes 0;
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Homo sapiens, close IMAGE:4749735, mRNA.
BC034824
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
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100.0%; Pred. No. 3.3
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                            Email: genexpress@genethon.fr
Single read.
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                                                                                                           and its expression
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hes 75; Conservative
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95277534
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Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 52 Row: d Column: 19
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                                                                                                                                                                                                                                                                                                                                                                                       This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5915657 This clone has the following problem: incomplete processing. Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 998)
NIH-MGC http://mgc.nci.nih.gov/.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arcayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center code: SOW HGSC
Center code: SOW HGSC
Contact: amg@bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
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Email: ccapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: KGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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/db_xref="taxon:9606"

/clone="IMAGE:474975"

/clone=lib="NoI_CGAP_Sxn4"

/lab_host="NoI_CGAP_Sxn4"

/note="Vector: pckv-Sporr6.ccdb"

a 234 c 230 g 234 t
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Pred. No. 3.7e-08;
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100.0%; Pred. No. J...
'... 0; Mismatches
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/db_xref="taxon:9606"
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Location/Qualifiers
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Plate: LLAM10503 row:
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BG678861
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/clone_lib="G"
/note="Genoscope
106 c 80
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CNS04M2X
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                                  Q \overline{Y}
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                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster genome survey sequence SP6 end of BACN15123 of DrosbAC ibrary from Drosophila melanogaster (fruit ALI), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-JUJ-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (3-mail : seqrefégenoscope.cns.fr ... Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.w - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPE (Centre d'Etude du Bolymorphisme Humain) with funding provided by a MRC and Genevieve Payan. It has been constructed in the vector
                                                                ; Site_1: NotI; Primer: Cligo dT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391 GAGIGGGGCCGGGACCCGCAGAGCCGAGCCGACCCITCTCTCCCGGGCTGCGGCAGGGCA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGTCTTAGGCCGGCGCCCCGGGGGGGAAGGGGAACGCAGACCCGGGACCCGTAAGACA 124
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/lb.host="NHOB6 (TI phege-resistant)"
/note="oran" skin; Vector: pcMV-SPORT6; Site_1: Not.
Site_2: Sall; Cloned unidirectionally. Frimer: Oligg
Average insert size 1.5kb. Library constructed by 3
rechnologies. Note: this is a NCI_CGAP Library."
2 233 c 244 g 236 t
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Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1201)
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41.0%; Pred. No. 0.0024;
tive 34; Mismatches 97; Indels 0;
                                                                                                                                                                               Length 998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN15123"
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Pred. No. 0.00015;
0; Mismatches 8
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/clone="IMAGE:4749735"
/clone_lib="NCI_CGAP_Skn4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
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                                                                                                                                                                               13.0%;
89.0%;
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                                                                                                                                                                                                                                                                                                                                           61 GGGGGGGGAGCTC 73
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Best Local Similarity
Matches 65; Conserv
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Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
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Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetraodontidae, Tetraodon.

1 (bases 1 to 298)

2 (bases 1 to 298)

2 (bases 1 to 298)

2 (bases 1 to 298)

3 (bases 1 to 298)

4 (bases 2 to 298)

5 (bases 2 to 298)
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Tetraodon nigroviridis DNA sequence
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                                      CNSO4M2X

Tetraodon nigroviridis genome survey sequence T7 end of clone
119N17 of library G from Tetraodon nigroviridis, genomic survey
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Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,
Weissenbach,J.
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                                                                                                                             185 GGGGGTGAACGTCGCCGGTTTAAGGGGGGGGGCCCGGCTCC 226
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/db_xref="taxon:99883"
/clone="119N17"
                                                                                                                                                                    1107 GGGGGGSGSGSCGNGGGGCSGGGSGCSSGSSGSCCCGGSCSC
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AL296898.1 GI:8035478
GSS; genome survey sequence.
Tetraccon nigroviridis.
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388 AGIGAGIGGGGCCGGGACCCGCAGACCGGACCGACC 424
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                                                                                                                                      Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                             Eukaryota, Metazca, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     575 GGKKAKGGVRGGRVCCAGGGASCACMAADCGGCCAKMACCSSSSASSSGSSCASTSSSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        795 GVSSGSSCSASCGSCCGVSSCSAVSASSASSVMSKVASAVASCBAVASGMSAGAVSSSCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 AGGGGCGGGCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAACAGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                915 VVSSSSSSSSSSASVVVSASVAASASSVSSSSSSVSTSSSASVSSVSAVSMSAVVSSS
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/db_xxref="taxon:7227"
/db_axx Fa="taxon:7227"
/clo.mc_lib="Drosbac"
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13.4%; Pred. No. 0.
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                                                                                                                                                                                                                                                                                             Drosophila melanogaster
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AL103460
AL108460.1 GI:5628764
               181 CGTGGGCGGCTGAACGTCG 199
                                     263 GGGGGGGGGGGGGGGG 281
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Signature of the control of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org.The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and malanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Marmoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. NY. The ibrary is named RPCI-98 and was constructed by partial Econt digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://wacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                   925 bp DNA linear GSS 03-JUN-1999
ter genome survey sequence IET3 end of BAC #
library from Drosophila melanogaster (fruit
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Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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1035 SVSSVSSSSCSVVSVVSSSSVSVAVASASASASVSSV 1071
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ilarity 14.3%; Pred. No. 0.12;
Conservative 116; Mismatches
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AL053013
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/clone_lib="RPCI-98"
/note="end : IET3"
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Drosophila melanogaster
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BACR19D16 of RPCI-98
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AUTHORS JOURNAL

COMMENT

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KEYWORDS

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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EYRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) -
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN17N07 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                        Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (BDPP) thtp://www.edgo.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CBPH (Centre European Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CBPH (Centre European Project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                 Direct Submission (23-010-1999) Genoscope - Centre National de Sequencage BP 191 9106 FWRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr Web : www.genoscope.cns.fr)
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Epnydroidea: Drosophilidae; Drosophila.
                                                                     Neoptera, Endopterygota, Diptera; Brachycera, Muscomorpha;
Ephydroidea, Drosophilidae, Drosophila.
1 (bases 1 to 1009)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/db_xref="taxon:727"
/clone="BACN03;19"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
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Web: www.genoacope.ons.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila denome Project (BDGP).

The BDGP is constructing a prysical map of the Drosophila melanogaster genome using these BACs. For further information: please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Marmoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-96 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.ouffalo.edu/drosophila_bac.thm.
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CNSCO6EZ B70 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR13E15 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 ACACCTGCTGTACCCTCCACCCCACCCCACCACCTCCCCCCAACTCCCTAGATGTGTC 181
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                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                     Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Eptydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         621 MGSSGGNGIGGYCCYCSCTCTCCSCYSCGCGCSGYNCSCSCCSCSCSY 571
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/db_xref="taxon:7227"
/cione="BACR13E15"
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                                                                           fly), genomic survey sequence.
AL064271
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/note="end : TET3"
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                                                                                                                                                                                    Drosophila melanogaster.
Drosophila melanogaster
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GSS.
                                                                                                                                  AL064271.1 GI:4944346
                                                                                                                                                                                                                                                                                              Ephydroidea; Drosog
1 (bases 1 to 870)
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es 63; Conserv
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Droscophila melanogaster genome survey sequence SP6 end of BAC
BACN37L10 of DrosBAC library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre CELtdée de Polymorphisme Humain) with funding provided by a KRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       οĘ
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Determination of this BAC-end sequence was carried out as part
Collaboration with the European Drosophila Genome Project (EDGP
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1097 SCSCGSCCCSCBBTCSSCRSSSCSMMSSVSCSVVCVASVCVCVGVMVTMGVSDGRBRDV 1038
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVSSSSCVCCSSVBCSCTSYCSSCSCSCCCCCCCCCASCRCRSMSMVMSMVASMTT
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Ephydroidea, Drosophilidae, Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                                                    Length 1101;
                                                                                                                                                                                                                                                                                                                   415 others
                                                                                                                                                                                    melanogaster'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.3%; Score 47.6; 19.1%; Pred. No. 0.
                                                                                                                                                                             /organism="Drosophila
/db_xref="taxon:727"
/clone="BACN17N07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fly), genomic survey sequence. AL108536
AL108536.1 GI:5628840
                                                                                                                                                                                                                                                                       /plasmic="pBeloBAC11"
/note="end : 5P6"
                                                                                                                                                                                                                                                /clone_lib="DrosBAC"
                                                                                                                                      occation/Qualifiers
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209 q
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Direct Submission 1999) Genoscope - Centre National de Sequencage : By 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDG?).

The BOGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecozidagestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacapec.med.ouffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNSGOCS1 843 bp DNA linear GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR26H19 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
library (Dros BAC) was made by Alain Billaud at CEPH (Centre C'Etude ou Folymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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1. (bases 1 to 843)
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                                                                                                                                                                                                                                                                                                                              179 others
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/db_xref="taxon:7227"
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/organ="Drosophila melanogaster"
/db.xref="taxon:7227"
/clone="BACN37L10"
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                                                                                                                                                                                                                                                                                                                                                                                                                              0.19;
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AL059666
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/plasmid="pBeloBAC11"
/note="end : SP6"
                                                                                                                          Location/Qualifiers
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Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                 42.9%;
                                                                                                                                                                                                                                                                                                                              174 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                        57; Conservative
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Direct Submission
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                                                           Query Match 10.2%; Score 47; DB 17; Length 843; Best Local Similarity 40.5%; Pred. No. 0.23; Matches 56; Conservative 22; Mismatches 60; Indels
                         210 others
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/clone_lib="RPCI-98"
/note="end : TET3"
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Les 86; Conservative
                                                                          4181
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CLASSIFICATION:
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MOLECULE TYPE:
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US-09-041-886-18
                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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Query Match
Best Local Si
Matches 85;
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Sequence 1, Appl.
Sequence 1, Appl.
Sequence 7, Appl.
Sequence 9, Appl.
Sequence 9, Appl.
Sequence 1, Appl.
Sequence 1, Appl.
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6534.056 Million cell updates/sec
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                                                                  ; Search time 21.7309 Seconds
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Sequence 1,
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-483-533-38
US-09-283-471A-38
US-07-841-646-3
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US-08-483-533-36
US-09-283-471A-36
PCT-US91-06532-1
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US-09-103-840A-1
US-08-306-691B-19
PCT-US93-06251-19
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US-08-018-977C-4
US-08-804-227C-1
US-08-072-574-7
US-08-072-574-9
                                                                                                                                                                                         of hits satisfying chosen parameters:
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US-08-447-570-3
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US-08-765-907A-
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US-08-664-855-1
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                                                                                                                                                                        441362 segs, 153338381 residues
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                                                                  3, 2003, 12:56:40
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                                                nucleic search, using sw model
                                                                                                                                            IDENTITY_NUC Gaport 2.0
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Match
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Seguence 56,
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Sequence 7
Sequence 7
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52.1%; Pred. No. 0.43;
live 0; Mismatches 79; Indels 0
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s of Use
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRAN APPLICATION NATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Campbell & Flores LLP 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Proapoptotic Peptides, De
TITLE OF INVENTION: Polypeptides and Methods
NUMBER OF SEQUENCES: 72
US-08-964-127-3
US-09-496-692-3
US-08-964-127-15
US-08-964-127-15
US-08-496-692-1
US-08-496-692-1
US-08-153-757-7
US-08-153-757-7
US-08-153-757-9
US-08-150-188-3
US-08-188-3
US-08-660-148-3
US-08-650-148-3
US-08-650-148-3
US-08-650-148-3
US-08-650-148-3
US-08-650-148-3
US-08-650-148-3
US-08-650-148-3
US-08-650-148-3
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Patent No. 6235872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGERATION NUMBER: 31,815
REPERENCE/COCKET NUMBER: P-LT
TELECOMMUNICATION INFORMATION:
TELEPAK: (619) 535-9901
TELEPAK: (619) 535-9949
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
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nucleic acid
EDNESS: single
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United States
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61 ccgcgcgrcfTaggcccgcgccccggcggggggaggggacgcagaccgcggagccTaa 120
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121 GACACCTGCTGCTCCACCCCCACCC---CACCCACCTCCCCCAACTCCCTAGATG 177
                        289 CCACCIGGIGGICTGGGCCTCGGCCCCCCTGGCGCCCCGCGCTCGTGGGCCCGCGA 348
                                                                            178 TGTCGTGGCGGCTGAACGTCGCCCGTTTAAGGGGCGGGCCCCGGCTCCACGTGCTTTCT 237
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APPLICANT: Chou, Joany
TITLE OF INVENTION: Method For Treating Tumorigenic Diseases
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49.6%; Pred. No. 0.34;
tive 0; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 5300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOPTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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04-APR-1999
... 514
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COUNTRY: United States of America
CONPUTER READABLE FORM:
AMEDIUM TYPE: REAPRY disk
COMPUTER: IBM PC comparible
OPERAIING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Figure Dense.
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR TOTAL NUMBER: 07/861,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/861,233
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA: 4APLICATION NUMBER: 08/415,853
FILING DATE: 11-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/483,533
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09283471A Patent No. 6340673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FELECOMMUNICATION INFORMATION:
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nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                    349 GCGGGCCGACCGGGCT 364
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                                                                                                                                                               238 GCTGAGTGACTGAACT
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STREET: 500
TTTV: Chicago
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        GTCTTAGGCCGGCGCGCCGGGGGGGAAGGGGACGCAGACCGCGGACCCTAAGACACC 126
                                                                                                       254 ICCAGCGGCCGGCGCGGCGGAGCGGGCGGGCGGCGGCGCGCGCGCCCCGGGACCGTAIC 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                      Method for Treating Tumorigenic
Diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 126;
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COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,533
FILING DATE: 07-MAR-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                    US-08-483-533-4; Sequence 4, Application US/08483533; Patent No. 6172047; Patent No. 6172047
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IELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 31-MAR-92
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, James P.
REGISTRATION NUMBER: 28,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 07-MAR-95
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/4'
FILING DATE: 11-APR-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 595 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 49.65
Matches 127; Conservative
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Roizman, Ben
APPLICANT: Chou, Joany
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Mêt
TITLE OF INVENTION: Dis
NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
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CITY: Chicago
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61 COGCGCGTCTTAGGCCGGGCGGGCGGGGGGAAGGGGACGCAGACCGCGGGACCCTAA 120
                                                                                                 121 GACACCTGCTGTACCCTCCACCCCACCC --- CACCCACCTCCCCCCAACTCCCTAGATG 177
                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                      Sequence 36, Application US/09283471A
Patent No. 6540673
GENERAL INFORMATION:
APPLICANT: Rolzman, Bernard
APPLICANT: Chou, Joany
TILLE OF INVENTION: Method For Ireating Tumorigenic Diseases
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CORRENT APPLICATION NUMBER: US/09/283,471A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.3%; Score 38.4; DB 4;
49.6%; Pred. No. 0.39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 27373/32742A IELECOMMUNICATION INFORMATION:
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STATE: lilinois
COUVERY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/861,233
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/419,853
FILING DATE: 11-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/483,533
FILING DATE: 07-307-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28,491
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312/474-0448
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LENGTH: 1327 base pairs
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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Best Local Similarity 49.6
Matches 127; Conservative
                                                                                                                                                                                                                                                                        790 GCGGCCGACCGGGCT 805
                                                                                                                                                                                                                                    238 GCTGAGTGACTGAACT 253
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SDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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STREET: boc.
TTV: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) TOPOLOGY: li
) MOLECULE TYPE:
US-09-283-471A-36
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                                                                                                                                      178 TGTCGTGGGGGGGGGGGGGGCCCGTTTAAGGGGGCGGGGCCCGGGTTCGACGTGCTTTCT 237
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                                                           GACACCTGCTGTACCCTCCACCCCACCC --- CACCCACCTCCCCCAACTCCCTAGATG 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ITLE OF INVENTION: Method for Treating Tumorigenic IITLE OF INVENTION: Diseases NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CALLCATION NUMBER: US/08/483,533
FILING DATE: 07-MAR-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125
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49.6%; Pred. No. 0.39;
ative 0; Mismatches 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA
APPLICATION DATA:
FILING DATE: 11-APR-95
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 31-MAR-92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                      Sequence 36, Application US/08483533 Patent No. 6172047
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TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MCLECULE TYPE: DNA (genomic)
US-08-483-533-36
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Roizman, Bernard
APPLICANT: Chou, Joany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1327 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                              349 GCGGCCGACCGGCT 354
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REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 07 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-3856
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                                                                                                                                                                                                                                                                                                                 RESULT 4
US-08-483-533-36
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725 GAGGGGGGGGGCGCGCGGGGAGGGCCCGTGCCACCTCCACGCCCGGCCCCCCGAGCCG 666
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                                                                                                    Weber, Peter C.
FENTION: DNA Sequences Encoding Mutant Antiviral
FENTION: Regulatory Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.1%; Score 37.6; DB 1; Length 936; larity 54.3%; Pred. No. 0.58; Conservative 0; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette, 3.50 inch, 720 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA Sequences Encoding Mutering OF INVENTION: Regulatory Proteins NUMBER OF SEQUENCES: 6 CORRESCENDENCE S. ADDRESSE: The Pennsylvania State University STREET: 113 Technology Center CITY: University Park STAIE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Microsoft Word for Windows 6.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/018,977C
FILING DATE: 18-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91-1039/2
                                                                                                                                                                                                                                                                                                         US-08-018-977C-4/c
; Sequence 4, Application US/08018977C
; Parent No. 5686601
; GENBRAL INFORMATION:
APPLICANT: Weber, Peter C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07/726,071
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REFERENCE/DOCKET NUMBER: 91-
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/726
FILING DATE: 05-JUL-1991
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 CCCACCTCCCCCCAACTCCC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPRONE: (814) 865-6277
TELEFAX: (814) 865-3591
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE IYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thomas J. Monahan
                                                                                                                                                                                                                             798 GCGGGCCGACCGGGCT 813
                                                                                                                                                                                      238 GCTGAGTGACTGAACT 253
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MEDIUM TYPE: Diskette
COMPUTER: IBM PS/2
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Best Local Similarity
Matches 76; Conserv
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                                                                                                                                             121 GACACCTGCTGTACCCTCCACCCCACCC---CACCCACCTCCCCCAACTCCCTAGATG 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant Herpes Simplex Viruses
Vaccines and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Roizzan, Bernard
TITLE OF INVENTION: Recombinant Herpes Simplex Vi
TITLE OF INVENTION: Vaccines and Methods
NUMBER OF SEQUENCES: 8
CORRESPENDENCE ADDRESS:
ADDRESSEE: Marchall, O'Toole, Gerstein, Murray
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentl: Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.3%; Score 38.4; DB 5;
49.6%; Pred. No. 0.39;
tive 0; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Two First National Plaza Suite 2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 27373/8235
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/346-5750
TELEPAX: 312/984-9740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MBER: PCT/US91/06532
19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                   YT-US91-06532-1
Sequence 1, Application PC/TUS9106532
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
ATTORNEYAGEN: INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 49.69
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                              238 GCTGAGIGACTGAACT 253
                                                                                                                                                                                                                                                                                                                                                   790 GCGGGCCGACCGGGCT 805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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TELERAX: 25-3856
TELEX: 25-3856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60603
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Db 18478 GCCACGCGTCGCGGGCACCGCCGAGCTCGCACTCCGCGACGGCACC 18526

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3273 CAGCGCCTTGGGGCCCTCTGGGGACTCGGGGCCGCCTGGGCCGCCTGCGCAGCC 3214
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APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen
APPLICANT: Liaw, Chen
APPLICANT: DATE-SEE ARON
TITLE OF INVENTION: HUMAN MATABOTROPIC GLUTAMATE RECEPTORS,
TITLE OF INVENTION: NOTLEIC ACIDS ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 CCCCCAACTCCCTAGATGTCTCGTGGGGGGGTGAACGTCGCCCGTTTAAGGGGCG 214
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                                                                                                                                                                                                                                                                                                                                                       B: Pretty, Schroeder, Brueggemann & Clark
444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35.8; DB 1;
Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "HUMAN MGLUR5A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/072,57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :: Floppy disk
IBM PC compatible
YSTEM: PC-DCS/MS-DOS
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Patent No. 5521297; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31.192
REFERENCE/COCKEI NUMBER: P41 9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-622-7760
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4.985 base pairs
                                                               Sequence 7, Application US/08072574
Patent No. 5521297
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Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM IYPE: Floppy
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STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                        STREET: 444 CONTRY: LOS Angeles
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OPERATING SYSTEM:
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Best Local Similarity
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CLASSIFICATION:
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                                                                                                                      GENERAL INFORMATION:
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                RESULT 9
US-08-072-574-7/c
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                                                                                                                        APPLICANT: DeHoff, Bradley S.
APPLICANT: Kussoos, Staarta A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
CORRESPONDENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/804,227C
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Floppy disk COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: MS-DOS SOFTWARE: ASCI(DOS) Text only CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/304,27 FLING DATE: FEDINAMINICALION TO THE OPEN THE OPEN
                                                                                                                                                                                                                                                                                                        E: THOMAS G. PLANT 1501
LILLY CORPORATE CENTER
                                         Sequence 1, Application US/08804227C Patent No. 5876991 GENERAL INFORMATION:
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NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
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TYPE: nucleic acid
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36249..41774
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14351..19945
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20010..31199
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Best Local Similarity
Matches 86; Conserv
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TOPOLOGY: li
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LOCATION:
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FEATURE:
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US-08-804-227C-1
RESULT 8
US-08-804-227C-1
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NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                             STATE: California
                                                                                                                      USA
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US-09-103-84CA-1
                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                  COUNTRY:
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SEQ ID NO 1
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TRANSLOCATION BREAKPOINT ASSOCIATED WITH ACUTE LEUKEMIAS
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APPLICANT: Daggett, Lorrie
APPLICANT: Ellas, Steven 3.
APPLICANT: Law, Chen
APPLICANT: Law, Chen
APPLICANT: Pontsler, Aaron
TITLE OF INVENTION: HUMAN MAIABOTROPIC GLUTAMAIE RECEPTORS,
TITLE OF INVENTION: NUCLEIC ACIDS SNCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 13
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                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,574
FILING DATE: 19930604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 370..4008
OTHER INFORMATION: /product= "HUMAN MGLUR5B"
OTHER INFORMATION: /note= "Variant of MGLUR5
                                                                                                                                                             ADDRESSE: Pretty, Schroeder, Brueggemann & STREET: 444 Scuth Flower Street, Suite 2000 CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Reiter, Stephen E. REGISTRATION NUMBER: 31,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P4 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 213-622-7700
TELEPAX: 213-489-4213
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4181 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Evans, Gien A. APPLICANT: Djabali, Malex APPLICANT: Select, Licia APPLICANT: Parry, Pauline TITLE OF INVENTION: TRANSLO TILLE OF INVENTION: TRANSLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: COS
                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                    STATE:
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASE, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 ACCTCCCCCCAACTCCCTAGATGIGTGGGGGGGGGGGGTGAACGTCGCC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 GCCGCCCCCCGGTGGTCCCGGGTCGGGGGGGAAGCGCCACC 17
           Schroeder, Brueggemann & Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             827
                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
ADDRESSEE: Pretty, Schroeder, Brueggemann & STREEN: 444 South Flower Street, Suite 2000 CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35.8; DB Pred. No. 2.6; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                  NAME: Reiter Stephen E.
REGISTRATION NUMBER: 31.192
REFERENCE/DOCKET NUMBER: P41 9387
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                     UMBER: US/08/061,376
13-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRGANISM: Mycobacterium tuberculosis
CTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: I3M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.7%;
Best Local Similarity 50.9%;
Matches 85; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (619)546-4737
TELEPAX: (619)546-9392
INFORMATION FOR SEQ ID NO: 4.5
SEQUENCE CHARACIERISTICS:
LENGTH: 11907 base pairs
                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patenti: Ver. 2.1
                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy
                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
FILING DATE: 13-MAY
CLASSIFICATION: 435
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LENGTE:
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                                                                                     Db 1630671 CACCGCCCCCCCCCCCCCCGCGCTGCCGTGGACCCCGGGCTACCGAGGC 1630730
                                                                                                                                                         0
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APPLICANT: Skorski, Tomasz
TIELE OF INVENTION: ANTISENSE
TIELE OF INVENTION: OLIGONUCLEOTIDES TARGETING COCPERATING ONCOGENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 GOAGACCGGGGACCCTAAGACACCTGCTGTACCCTCCACCCCCACCCCACCCTCCCC 162
                                                                                                                                       APPLICANT: FISISCEMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DAM SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCLIOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                    Gaps
                                                                   Score 35.6; DB 4; Length 4411529; Pred. No. 8.2; 0; Mismatches 54; Indels 0;
DB 4; Length 4411529;
                                  0
                                65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Seidel, Gonda, Lavorgna & Monaco, P.C.
Two Penn Center, Suite 1806
Score 35.6; DE
Pred. No. 8.2;
0; Mismatches
                                                                                                                                                                                                                                           Db 1630791 geccaccegrecaccegrece 1630812
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; OTHER INFORMATION: H37Rv
US-09-103-846A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/08305691B
Patent No. 5734039
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
                                                                                                                                                                                                            160 CCCCCAACTCCCTAGATGTGTC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.7%;
 7.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 55.7
Matches 68; Conservative
Query Match
Best Local Similarity 54.2
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
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US-08-306-691B-19/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 836329 CC 836328
                                                                                                                                                                                                                                                                                                  RESULT 13
US-09-103-840A-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 CC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8471 cerececcanecerrerenerececentacarcercaracarcarcarcaracerrangegrang 8412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 CIAAGACACCTGCTGTACCCTCCACCCCCACCCCACCCACCTCCCCCAACTCCCTAGAT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 CTTCCCGCGCGTCTTAGGCCGGGGGGGGGGGGGGGAAGGGGAAGGCGACGCAGGGGACC 11.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 GTGTCGTGGGCGGCTGAACGTCGCCCGTTTAAGGGGGCGGCCCCGGCTCCACGTGC 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 35100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US93/06251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35.2; DE Pred. No. 4.5; 0; Mismatches
        3: Diskette, 3.50 inch, 720 kb
IBM PS/2
                                                                                                                       US/08/305,691B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application PC/TUS9306251
GENERAL INFORMATION:
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                                                                                                                                          September 15, 1994
1: 514
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ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"""TER: IBM PC COMpatible
"""" PC-DOS/MS-D"
                                                                                                                                                                                                                                                                                     30,480
                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 83:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                               TELEPAONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5734(039e
INFORRATION FOR SO ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.6%;
                                                                            SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C8/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNET/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      35100 base pairs
                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                           OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                  NAME: Monaco, Daniel A. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 400 City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1 CLASSIFICATION:
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                                                                                                                                             FILING DATE:
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US-08-306-6913-19
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REFERENCE/DOCKEI NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHORE 516-742-434
TELEPAX: 516-742-436
TELEPAX: 33 091 SANS UR
TELEPAX: 33 091 SANS UR
INFORMATION FOR SED ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENTH: 35100 base pairs
TYPE: nucleic acid
STRANDED/SES: double
STRANDED/SES: double
TYPE: nucleic acid
STRANDED/SES: double
TYPE: nucleic acid
STRANDED/SES: double
STRANDED/SES: double
TYPE: nucleic acid
TYPE: nucleic acid
STRANDED/SES: double
TYPE: nucleic acid
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Search completed: February 3, 2003, 21:01:05 Job time: 7799.73 secs

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(without alignments)
7959.555 Million cell updates/sec
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1: /cgn2_6/gtodata/1/pubpna/NCT_NEW_PUB.seq:*
2: cgn2_6/gtodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/gtodata/1/pubpna/NCG0_NEW_PUB.seq:*
4: /cgn2_6/gtodata/1/pubpna/USO0_NEW_PUB.seq:*
5: /cgn2_6/gtodata/1/pubpna/USO0_NEW_PUB.seq:*
6: /cgn2_6/gtodata/1/pubpna/USOB_NEW_PUB.seq:*
7: /cgn2_6/gtodata/1/pubpna/USOB_NEW_PUB.seq:*
8: /cgn2_6/gtodata/1/pubpna/USOB_NEW_PUB.seq:*
9: /cgn2_6/gtodata/1/pubpna/USOB_NEW_PUB.seq:*
10: /cgn2_6/gtodata/1/pubpna/USOB_NEW_PUB.seq:*
11: /cgn2_6/gtodata/1/pubpna/USOB_NEW_PUB.seq:*
11: /cgn2_6/gtodata/1/pubpna/USOB_NEW_PUB.seq:*
13: /cgn2_6/gtodata/1/pubpna/USOB_NEW_PUB.seq:*
14: /cgn2_6/gtodata/1/pubpna/USOB_NEW_PUB.seq:*
13: /cgn2_6/gtodata/1/pubpna/USOB_NEW_PUB.seq:*
14: /cgn2_6/gtodata/1/pubpna/USOB_NEW_PUB.seq:*
14: /cgn2_6/gtodata/1/pubpna/USOB_NEW_PUB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396772 seqs, 224632407 residues
                                                                                                                                                                                                                                                                                                                                          US-09-596-141C-3_COPY_1181_1643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                            OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                             Seguence:
                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                              Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 44, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 1, Appli Sequence 1386, Appli Sequence 1, Appli Sequence 3381, Ap Sequence 2587, Ap Sequence 3, Appli Sequence 2109, Ap Seguence 250, App Sequence 987, App Sequence 1003, Ap Sequence 1012, Ap Seguence 1024, Ap Description US-09-772-304A-1 US-09-633-301-1386 US-09-834-975-1003 US-09-834-975-1012 US-09-834-975-1012 US-09-834-975-1012 US-09-814-975-1012 US-09-814-975-1012 US-09-814-876-2109 US-09-923-876-250 US-09-998-258-2587 US-09-898-588-2587 US-09-898-588-2587 US-09-846-456-3 0 US-09-846-456-3 0 US-09-815-048-3 0 US-09-815-048-3 US-10-047-542-44 US-09-799-562A-17 US-10-125-767-17 SUMMARIES 10 10 10 10 10 10 Query Match Length DB 10000 Score Result Ñ. 0000000000

Sequence 39C, App Sequence 390, App	3, Appl	(1)		d1		Sequence 17, Appl	, App	176,	Seguence 9, Appli	, App	C1	ດ	3950,	6, App	Sequence 6, Appli	ďďY ′	(T)			91	\circ	σ	Sequence 1, Appli	Sequence 3. Appli
US-09-854-133 0 US-09-738-97	US-10-000-273-3	0 US-09-833-381	US-10-000-	US-05-770-689A	US-09-799-452A-1	US-10-125-767-1	US-10-199-333-1	US-09-860-35	55-830-	US-09-373-967-	0 US-09-954-456-2	0 US-09-954-456-52	0 US-09-880-107-	US-10-125-470-6	US-10-125-452-	0S-08-822-20	0 US-09-917-80	0 US-09-954-456-	96-60-SD	US-10-044-090-5	-783-590-	US-09-764-870-1	US-09-899-634A	10 US-09-835-081-3
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20	22	23	24	25	26	27	28	58	m	m	m	m	m	(C)	(11)	(*)	(7)	39	40	41	42	43	4	7
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ALIGNMENTS

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TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying TITLE OF INVENTION: Activity and Therapeutic Uses FILE REFERENCE: 3806.0505 CURRENT APPLICATION NUMBER: US/09/846,456 CURRENT FILING DATE: 2001-05-02 PRIOR PELICATION NUMBER: US 60/201,280 PRIOR FILING DATE: 2000-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2636
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                Sequence 1, Application US/09846456 Patent No. US20020146792A1
                                                                                                                                                                                                                                                                                                                                                                                                          version 3.0
                                                                                                              Lemoine, Cendrine
Naudin, Laurent
Denefle, Patrice
                                                                                                                                                                         APPLICANT: Duverger, Nicolas APPLICANT: Brewer, Sryan APPLICANT: Remaley, Alan APPLICANT: Fojo, Silvia
                                                                             APPLICANT: Rosier, Marie APPLICANT: Prades, Catherine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn
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US-09-846-456-1
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APPLICANT:
APPLICANT:
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APPLICANT: Fojo, Ŝilvia
TITLE OF INVENITON: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying
TITLE OF INVENITON: Activity and Therapeutic Uses
FILE REFERENCE: 3806.0505
CURRENT APPLICATION NUMBER: US/09/846,456
CURRENT FILING DATE: 2001-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/C9815048
Patent No. US20020:37131A1
GENERAL INFORMATION:
APPLICAMY: WEL, Ming-Hul et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001180 NDMBER: US/09/815,048
CURRENT APPLICATION NUMBER: US/09/815,048
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 4
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1.3e-15;
hes 0;
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100.0%; Pred. No. 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/201,260
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                  Sequence 4, Application US/09846456 Patent No. US20020145792A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin version 3.0
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Lemoine, Cendrine
Naudin, Laurent
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Duverger, Nicolas
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Remaley, Alan
Fojo, Silvia
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 42450
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US-09-815-048-3
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: Acidity and Therapeutic Uses
FILE REFERENCE: 3806.0505
COURENT APPLICATION NUMBER: US/09/846,456
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/201,280
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                 296 ACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAAICTATAAAAGGAACTA 355
                                                                                                                                                                                                                                                    1 CCITEGCTECCEGGAACGTEGACTAGAGACTCTECGECGCAGCCCCGAGCCCAGCGCTTC 60
                                                 TGTGTCGTCGCCGCTCGCCCCTTTAAGGGGCGGCCCCGGCTCCACGTCCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09846456
Patent No. US20020146792A1
SERBEAL INFORMATION:
APPLICANT: Rosier, Marie
APPLICANT: Prades, Catherine
APPLICANT: Lemoine, Centrine
APPLICANT: Naudin, Lemoine, Centrine
APPLICANT: Naudin, Laurent
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Duverger, Nicolas
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APPLICANT: Remaley, Alan
APPLICANT: Fojo, Silvia
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US-09-846-456-3
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 GAACGTGGACTAGAGAGTCTGCGGCGCAGCCCCAGCGCTTCCCGCGCGTCTTAG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hadlaczky, Gyula
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES IHEREOF AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 COCTCCACCCCACCCACCCACCCCCCCAACTCCCTAGA 175
             CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37.2; DB 9;
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24601-402G
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/799,462A FILING DATE: 10-Sep-2001 CLASSIFICATION: <UNKnown>
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                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/835,682
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-AUG-1956
APPLICATION NUMBER: 08/682,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 15-JUL-1995
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-APR-1996
                                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stephanie L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 42999 base pairs TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHODS
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MOLECULE TYPE: Genomic DNA
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INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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Best Local Similarity 51.94
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Seidman,
                                                                                CITY: La Jolla
                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE:
                                                                                                       STATE: CA
                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-125-767-17
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Szalay, Aladar
TITLE OF INVENTION: ARTHORM FOR PREPARING ARTIFICIAL CHROMOSOMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: LARRICK, JAMES W.
APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: WOUNDE IMMUNABHERINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISSASES
FILE REFERENCE: 039905.0004.CIP1
                                                                                                                                                        1537 GGCTCCCGGGACGCAAGCCTCTAGAGGGCGCGGAGGCCCCGCCCCGCCCTTCGGCC 1596
                                                                                                                                                                                                                                         167 CICCCIAGAIGIGICGIGGGCGGCIGAACGICGCCCGTTTAAGGGGCGGGCCCCGGCTCC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             628 TTCACCCCCCCACCGTGAAGAICTTACAGTCGTCCTGCGACGGCGGCGGCGACTTCCCC 687
                                                                                                                                                                                                              65 GCGICTTAGGCCCGGGGCCCGGGGGGGGAGGGGACGCAGACCGCGGACCCTAAGACA 124
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                                                                                     Gaps
                                                                                                                           5 GGCIGCCGGGAACGTGGACTAGAGAGTCTGCGGCGCAGCCCCGAGCCCAGCGCTTCCCGC 64
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                                      Length 42450;
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                                                                                  Indels
                                                                                                                                                                                                                                                                                                 COTGOTGTACCOTGCACCCCACCCACCCACCTCCCCCCAACTCCC 171
                                      Score 37.4; DB 10;
Pred. No. 0.95;
0; Mismatches 81;
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Pred. No. 0.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/047,542 CURRENT FILING DATE: 2031-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US01/13932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/09799462A Patent No. US20020160970A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-04-28
PRIOR APPLICATION NUMBER: 60/200,298
PRIOR FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 44, Application US/10047542
Patent No. US20020168367A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch
1 Similarity 49.5%;
96; Conservative 0
                                        9.1%;
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                                                                                     Conservative
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Best Socal Similarity
                                                              Similarity
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                                      Query Match
Best Local Simil
Matches 86; (
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US-10-047-542-44
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US-09-815-048-3
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TITLE OF INVENTION: NOVEL ESCHERICHIA COLI HAVING ACCESSION
TITLE OF INVENTION: NO. PTA 1579 AND ITS USE TO PRODUCE POLYHYDROXYBUTRATE
FILE REPERENCE: A33943 066123.0103
CURRENT APPLICATION NUMBER: US/99/772,304A
CURRENT FILING DATE: 2001-61-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INFUNITON: No. US20020132090Aiel Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        947 GCCGGCCACCAGGGGGGAGCACCAGGGCCGGGCGGGCAGCTCCGAGGGCAGGGTCG 888
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                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                       7.9%; Score 36.6; DB 10; Length 4826; 49.7%; Pred. No. 0.91;
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Live 0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                     NUMBER OF SEQ ID NOS: 1 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1386, Application US/09833382
Patent No. US20020132090A1
                                                                                                                                                                                                                                                                             ORGANISM: Streptomyces aureofaciens
                                                                                                                                  2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)...(1102)
; CIEER INFORMATION: n = A,T,C or
US-09-833-381-1386
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Tripatii, G.
Ramchander, T.V.N.
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Best Local Similarity 51.2
Matches 109; Conservative
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                                            Rawal, S.K.
                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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LENGTH: 1102
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                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                SEQ ID NO 1
                                            APPLICANT:
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  FOR PREPARING ARTIFICIAL CHROMOSOMES
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                                                             ADDRESSEE: Heller Ehrman White & McAulliffe LLP STREET: 4350 La Jolia Village Drive, 7th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10133 ICCTCCCTCCTCCCCCACGCCCCCTCCCCCCCGGA 10174
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8.0%; Score 37.2; DB 9;
Best Local Similarity 51.9%; Pred. No. 1.1;
Matches 84; Conservative C; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Seidman, Stephanie L
REGISTRAATION NUMBER: 33, 779
REFERRNCE/DOCKET NUMBER: 24601-402J
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/125,767
FILING DATE: 17-Apr-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/724,693
FILING DATE: 28-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 17: US-10-125-767-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-AUG-1996
APPLICATION NUMBER: 08,682,080
FILING DATE: 15-JUL-1995
APPLICATION NUMBER: 08,629,822
FILING DATE: 10-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/835,682
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 42999 Jase pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       858-450-8403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 858-587-5360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <Unknown>
                                                                                                                                                                                       COMPUTER READABLE FORM:
                      NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                          CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mahishi, L.H.
                                                                                                                                                      USA
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FRAGMENT TYPE:
                                                                                                                           STATE: CA
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GENERAL INCOMMATION:
GENERAL INCOMMATION:
GENERAL INCOMMATION:
APPELICANT: Brown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Brown, Jeffrey
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
ITTLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, FOR THE DENTIFICATION.
TITLE OF INVENTION: OF HUMAN CANCERS
ITTLE OF INVENTION: OF HUMAN CANCERS
CURRENT APPLICATION NUMBER: 35/09/834,975
CURRENT APPLICATION NUMBER: 60/197,538
PRIOR APPLICATION NUMBER: 60/197,538
NUMBER OFFICE DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SEQ ID NOS: 1046
SEQ ID NOS: 1046
SEQ ID NO 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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49.0%; Pred. No. 1.3;
tive 0; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35.6; DB 10;
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 66/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOFWARRE: FastSEQ for Windows Version
SEQ ID NO 1003
LENGTH: 1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1012, Application US/09834975; Patent No. US20020110815A1
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; OTHER INFORMATION: n = A.I.C or
US-09-834-975-1012
                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)...(1797)
; OTHER INFORMATION: n = A,T,C or
US-09-834-975-1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 49.08
Matches 95; Conservative
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ORGANISM: Homo sapiens
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Matches 95; Conserv
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APPLICANT: Jille, James
APPLICANT: Drown, James
APPLICANT: Boot, Andrew
APPLICANT: Boot, Andrew
APPLICANT: Van Huffel, Christophe
APPLICANT: Van Huffel, Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Brown, Jeffrey
APPLICANT: BOLL, Andrew
APPLICANT: Wolf wildel, Christophe
APPLICANT: Van Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: OF HUMAN CANCERS
FILLE REFERENCE: MRI-016B
CURRENT APPLICANTON NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2006-04-14
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SOFTWARE: FastSEO for Windows Version 4.0
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Patent No. US20020110815A1
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; OTHER INFORMATION: n = A.T.C or
US-09-834-975-987
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APPLICANT: Lillie, James
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-834-975-987/c
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SEQ 1D NO 987
LENGTH: 1797
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GENERAL INFORMATION:
APPLICANT: Lalqudi, Raghurath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
IITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 GEGGGAAGGGGACGCAGACCCCGGACCCTAAGACACTGCTGTTACCCTCCACCCCCACCC 149
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Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442 SOFTWARE: Patentin Ver. 2.0 SEO ID NO 2109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
CTHER INFORMATION: Incyte ID NO. US20020013958A1 700156629H1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.4%; Score 34.4; DB 10; Best Local Similarity 52.8%; Pred. No. 1.7; Matches 65; Conservative 0; Mismatches 58;
                                                                                                                                                                                                     7.5%; Score 34.6; Di
55.4%; Pred. No. 4.2;
                                                                                                                                                                                                                                                  0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-06-21
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SEQ ID NO 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 250, Application US/09923876 Patent No. US20020013958A1
                                                                                                                                                                                                                             1 Similarity 55.4
57; Conservative
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US-09-764-869-2109
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CURRENT APPLICATION NUMBER: C6/197,538
PRIOR PILING DAIE: 2000-04-14
NUMBER OF SEQ ID NOS: 2046
SOFTWARE: FASCEQ for Windows Version 4.0
SEQ ID NO 1024
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    95 AAGGGGACCCAGACCGCGGGACCCTAAGACACCTGCTGTACCCTCCACCCCCACCCCACCCCACCC 154
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APPLICANT: Resen et al.
IIILE SOLIVENION: Nucleic Acids, Proteins, and Antibodies File Reference: PC007
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49.0%; Pred. No. 1.3;
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Patent No. US20020061521A1
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; Sequence 1024, Application US/09834975
; Patent No. US20020110815A1
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; OTHER INFORMATION: n = A,T,C or
US-09-834-975-1024
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APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
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ORGANISM: Homo sapiens
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US-09-764-869-2109/c
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Tue Feb 4 09:39:45 2003

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BQ67446 ACBNCOURT
BM411197 OP21284 M
AJ231825 Gallus ga
BAG77491 ACBNCOURT
ALIO6545 Drosophil
BF265654 HV_CE001
ALIO66745 Drosophil
ALIO66746 Drosophil
ALIO66746 Drosophil
ALIO67765 Prosophil
BQ2755 Fan trog1
ACO7355 Pan trog1
ALIO7751 Terracdon
BQ17838 UT M-ERO-
AL413725 T7 end of
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AL413725 T7 end of
AL72367 Drosophil
BC102367 Drosophil
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BF30384 601886514
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                       AL065629 Drosophil
AL05775 Drosophil
AL063713 Drosophil
AL063912 Drosophil
AL228688 Tetraodon
AL102515 Drosophil
BM415333 Op20407 M
AL580352 AL580352
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1532-3 Yana, Kisarazu, Chiba 252-0612, Japan
1532-3 Yana, Kisarazu, Chiba 252-0612, Japan
1532-3 Yana, Kisarazu, Chiba 252-0612, Japan
1538-52-3975
Fax: 81-438-52-396
Email: genomics@hrl.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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AG136883
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CNS0137T
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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                                                                                                                                                                                              .....cagggcagggcggggagctc 352
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                  GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                     16154066 seqs, 8097743376 residues
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                                                                                                                                                                   US-09-596-141C-3_COPY_1292_1643
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FEATURES

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Matches

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2 AATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGAGAGCCGAGCGGACCCTTCTCTCCC 61
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/note="Vector: pME18SFL3"
205 c 260 g 158 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Eomo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9506"
/clone="MAMMA1000851"
/clone_lib="MAMMA1"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 547)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Am Klopferspitz 18a D-82152 Kartinsried, Germany
This is the 5' sequence of the clone insert
Cione from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKTZ); Email S.wiemann@cKtz- heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the CDNA sequencing
consortium of the German Genome Project.
No Si sequence available:
This clone (DKTZp686N12109) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 5, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@trzpd.de.
1.547
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DKFZp686N12109_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686N12109 5', mRNA sequence.
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/clone_lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
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/note="Vector: pME18SFL3"
199 c 199 g 170
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/clone="PLACE1002437"
/clone_lib="?lACE1"
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Unpublished (1999)
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DEFINITION

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ACCESSION

VERSION KEYWORDS

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TITLE JOURNAL

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AUTHORS

REFERENCE

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Matches

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AU121731 AWMAI Homo sapiens cDNA clone MAMMAI000851 5', mRNA
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Marmalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 292)
                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 81-438-52-3986
Fax: 81-438-52-3986
Fax: Branches Edri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                            Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
EG-ix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
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Query Match
Best focal Similarity 100.(
Matches 75; Conservative
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/dev_stage="3 months old"
/dev_stage="develope="total brain"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, BureleosTomi,
Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,A.D., Duprat,S., Goulgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Kitchell,H., Kariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A. IMAGE: molecular integration of the analysis of the human genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single read.
Genexpress_library_idt: C: Genexpress_sequence_idt: ylc-lzb08
Seq primer: (-21)Ki3_universal.
Location/Qualiflers
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1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
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C. R. Acad. Scl. III, Scl. Vie 318 (2), 263-272 (1995)
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/sex="Female"
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9.6e-10;
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/db_xref="taxon:9606"
/clone="c-1zb08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genexpress@genetnon.fr
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Email: cgapbs-r@mail.nih.gov
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAK plate: 52 Row: d Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 5915657
This clone has the following problem: incomplete processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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                                                                                                                                                                                                                   Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Toon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.
Richards, S., Gibbs, R.A.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Central
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/clone_lib="NCI_CGAP_Skn4"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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1.1e-09;
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100.0%; Pred. No. 4...
... 0; Mismatches
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High quality sequence stop: 860.
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/db_xref="taxon:9606"
/clone="IMAGE:4749735"
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/db_xref="taxon:9606"
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Direct Submission
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of Collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruiffly.org The BDGP Drosophila melanogaster BAC library was prepared by KaZutoyo Googawa and Maron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalc, NY. The Library is named RPCI'S9 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on by Sp. the same strain used for the BDGP's Pl and ESI libraries. A more detailed description of the library
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         /clone_lib="NCI_CGAP_Skn4"
/clone_lib="NCI_CGAP_Skn4"
/tissue_type="scuamous_cell_carcinoma"
/lab_host="bulob (Tl_phage=resistant)"
/note="Organ: skin, vector: pGNV-SPORT6; Site_l: Not!;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                                                                                                                      280 GAGTGGGGCCGGGACCCGCAGAGCCGAGCCCATTCTTCTCCGGGGCTGCGGGCAGGGCA 339
                                                                                                                                                                                                                                                                                           Gaps
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Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                         17.1%; Score 60.2; DB 12; Length 998; 89.0%; Pred. No. 9.8e-05; Live 0; Mismatches 8; Indels 0;
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Drosophila melanogaster
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/db_xref="taxon:7227"
/clone="SACR19D16"
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/clone="IMAGE:4749735"
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/note="end : TEI3"
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

Web: iwww.genoscope.cns.fr)

Determination of this BAC-and sequence was carried out as part of

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see http://www.fruitfly.org The BDGP Drosophila

melanogaster BAC library was prepared by Kazutory Oscogawa and

Aaron Mammoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RRCI-98 and was constructed by partial

ECORI digestion of Drosophila DNA provided by the BDGP's

Pl and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library or

filters for hybridization from the BACPAC Resource Center can be

found at http://wardec.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 935)
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Pred. No. 0.37;
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/db_xref="taxon:7227"
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Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNSOU6ON 910 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14J21 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
- Neb : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                   211 GCGCTCGGTGCAGCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCGGTAATTGCG 270
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                                                                                                                                                                                                                        845 SGCGCCCSGSSCGCCCGSCGSCSCGGSCSCCGCGCCGSCSCGCGCGGCSGGCCSGGCGS 786
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neopiera; Endopterygota; Diptera; Erachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                           91 CGTTTAAGGGGCGGGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAAC
                   31 CCCCACCCCACCTCCCCCCAACTCCCTAGATGTGTGTGGGGCGGCTGAACGTCGCC
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Direct Submission
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Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencege :

BP 191 91006 EVENT cedex - FRANCE (E-mail : secref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Cosegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Castlitte in Buffalo, Nr. The library is named RPCI-98 and was constructed by partial Ecoki digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: or bw sp. the same strain used for the BDGP's Pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genome survey sequence TST3 end of BAC # BACR19016 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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872 CACRSSVCASAMGAASAGASAASASSSAVSACGSSSSSVSSVVSSASASASAGVSRSASS
                                                                                                                                                                                                                                                                          154 GGCCGGGAACGGGGCGGGGAGGAGGAGAACAACATTTGACCGATAGTAACCTCTGCG
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/close="BACR19D16"
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Score 39.6;

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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
Submitted (02-JUN-1999) FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                  83 ACGICGCCCGTTTAAGGGGCCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAACT 142
                                                                                                                                                                                                                                                                                                                                                              263 TAATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGGCCGAGCCGACCCTTCTCTC 322
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Drosophila melanogaster.
Drosophila melanogaster
Eukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota: Metazoa; Arthropoda; Brachycera; Muscomorpha;
                                                      SSSSSTSSSSTSKSSSSSSSSSSSTTTSKSTSASGSGSWSAGGGSGSTGSTSS
                                                                                                                                                                                                          203 TAACCTCTGGGCTGGTGCAGCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCG
                                                                                                                                                                                                                                                                                                                    CSCCTCCCSYSYSSSTSSSSSTSWGSTSGSSSSSVGTSSSSDSTSTCCSCCCYMCTCCST
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/db_xref="taxon:7227"
                  138;
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Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 912)
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                  Mismatches
  Pred. No.
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/clone_lib="RPCI-98"
/note="end : TET3"
a 240 c 82 g
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                  148;
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  12.58;
                  Conservative
Similarity
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collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Googawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer of Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is mamed RPCI-99 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2: on bw sp, the same strain used for the BDGP's Pland EST libraries. A more detailed description of the library and now to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be for a feature of the strain which the BACPAC Resource Center can be for the BACPAC Resource Center can be for the partial broads.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-JUN-1999) Genescope - Centre National de Sequencage : BP 191 91006 FPRX cedex - FRANCE (B-mail : segref@genoscope.cns.fr betermination of this BAC-end sequence was carried out as part of a
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Droscophia melanogaster genome survey sequence T7 end of BAC #
BACR08A10 of RPCI-98 library from Droscophila melanogaster (fruit
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                                                                                                                                                                         694 GGGGGVGSGVVSGGGGSSVVVRGRVGGGSGGGGGGVSCMVGNGMMGGGGVGMGGMGMSMGV 635
                                                                                                                                                                                                                                                                                           634 VVGMGVGMGMGGRGVGMGMMRRMRRCVAMGVGMGSSWCCSCMCMCGSGVGRGGSGVGSGC 575
                                                                                                                                                                                                                                                                                                                                                                                                             574 GMSAGASVGMSMGVGAGASRAASGMGCGCGCCCGCWCCCCCGCSCCCCCGCGSGRGGA 515
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoprera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                         found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
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/db_xref="taxon:7227"
/clone="BACR08A13"
                                                       76;
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                           ; Pred. No. 2.9;
67; Mismatches
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31.0%; Pred. No. 3.4;
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AL063912
AL063912.1 GI:4941769
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GAVASGCASGGGSRS 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 GCAGGGCAGGGCGGG 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene number estimate provided by genome wide analysis using Terraodon nigroviridis DNA sequence Unpublished
                                                                                                                                                                                                                                                                                                                                                            Fisher, C.,
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                                                                                                                                                 SMSAMSRCRCMCVMRGMSGCACCRVVMCGASGCRCRAMGGGACGMWVRAACRAGCVCSC 1055
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                            877 ACGCCYSVCRCGCCCACACCMRCMCCSVCGCSMSMGACAVWVMRAAGMRVGWRAMGARR 936
                                                                                        MGACRCRGRGRGAGSMRGSGVGGSGGCGSGGGGGGGGGGGGGGGGMRGGGGGGRSRGAGVM 996
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Roest-Crollius.H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 TAACCTCTGCGGTGCAGCGGAATCTATAAAAGGAACTAGTCCCGGCAAAAAAACCC
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/db_xref="taxon:99883"
/clone="213J04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38.8; DB 17;
Pred. No. 4.2;
34; Mismatches 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   GSS; genome survey sequence.
Tetraodon nigrovíridis.
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                                                                                                                                                                                                                                                                                                                                                    Tetraodon nigroviridis
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37.1%;
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GSS; cenome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                             Tetraodon
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton pBelobacii.
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Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
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                                                                                            90 CCGTTTAAGGGGCGGGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAA
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Ephydroidea; Drosophilidae; Drosophila.
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/organism="Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope.

Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
3P 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila
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/db_xref="taxon:7227"
/clone="BACR11P16"
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/note="end : TET3"
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completed: February 4, 2003, 03:26:48 He : 681.758 secs Job time

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                                                                                                                                                                                                                                                                               /note="Organ: breast; Vector: pucl8; Site_1: SmaI, Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 /716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and obNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
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1 (bases 1 to 467)

1 (Cash http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&t2=RC6-BT0252-271099-012-c10&t3=1999-10-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 146
High quality sequence stop: 289.
Location/Qualifiers
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ng37c02.s1 NCI_CGAP_CO3 Homo sapiens cDNA clone IMAGE:936962 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      798 ITTGITTCTTTTTTGTTTTTGTGGCCTCCTTCCTCTCAATTTATGAAGAGAAGAGTAA 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 TTTGTTTTTTTTTTTTTTTTTTTTTCTTCTTCTTCTCTTTATAATTTTTGAAGAAGCAGTAA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     858 GATGTTCCTCTCGGGTCCTCTGAGGGACCTGGGGAGCTCAGGCTGGGAATCTCCAAGGCA 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 CCTGCACTTCACAAATGTATACAAACTAAATACAAGTCCTGTGTTTTTATCACAGGAGG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         678 GCTGCACTICACAAATGTATACAAACTAAATACAAGTCCTGTGTTTTTATCACAGGGAGG 737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 GTAGGTCGCCTATCAAAAATCAAAGTCCAGTTTTGTGGGGGGAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 245.4; DB 10; Length
Pred. No. 6.3e-39;
0; Mismatches 6; Indels
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                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="3T0252"
/dev_stage="Adult"
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AU135588 PLACE1 Homo sapiens cDNA clone PLACE1002437 5', mRNA
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llof.gov/bbrp/image/thmige.html
Insert Length: 1167, Std Brror: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
sigh quality sequence stop: 380.
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Mammalia; Butheria; Primates; Catarrhini; Fominidae; Homo.
1 (bases 1 to 736)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genomics@nri.co.jp
HRI human cDNA project; 5'- 6 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ota'T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nekamura,Y., Nagai,T., Sugano,S. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            816 TTTGIGGCCICCTTCCICICALTTAIGAAGAGAAGCAGTAAGAIGTTCCTCTCGGGICC 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               876 ICTGAGGGACCTGGGGAGCICAGGCTGGGAATCTCCAAGGCAGTAGGTCGCCT 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 111.4; DB 9; Length 467; Pred. No. 3e-12; 0; Mismatches 1; Indels 0;
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
TTE: 81-438-52-3975
Fax: 81-438-52-3986
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                             /tissue_type="colon"
                                                                                                                                     Location/Qualifiers
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Contact: Takao Isogai
Genomics Laboratory
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99.18;
                                                                                                                                                                                                                                                                           /sex="pooled"
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244377
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Matches 89,
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                                                                                                                                                                                                                                                                                                                                         547 bp mRNA linear EST 21-MAR-2002
DKFZ2668M12109_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
AL698654
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Mammalia; Eutheria; Primates; Catarrhini; Eominidae; Homo.
1 (bases 1 to 547)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research Center (DKFZ); Emails submannedate, beidelberg, delicel sequenced by Qiagen (Hilden/Germany) within the CDNA sequencing consortium of the German Genome Project.

This clone (DKFZp686N12109) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcencentum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
                                                                                                                                                                             1553 GTAATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTC 1612
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                                                                                                         Length 736;
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                                                    5 others
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                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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/close_lib="686 (syponym: hlcc3)"
/close_lib="686"
/tissue_type="human skeletal muscle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.4%; Score 89; DB 9; Le Best Local Similarity 100.0%; Pred. No. 8.5e-08; Matches 89; Conservative 0; Mismatches 0;
                                                                                                   Score 89.4; DB 9;
Pred. No. 6.3e-08;
0; Mismatches 1;
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                                                    170 t
/clone_lib="PLACE1"
/tissue_type="placenta"
/note="Vector: pME18SFL3"
199 c 199 g 170
                                                                                                                                                                                                                                             1613 CCGGGCTGCGGCAGGCCGGGGGGGGCTC 1643
                                                                                                                                                                                                                                                                 61 CCGGGCTGCGCCAGGCCAGGGCGGGGAGCTC 91
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/lab_host="DH10B"
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EST (Duesterhoeft, et al.)
Unpublished (1999)
Contact: Duesterhoeft A
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Best Local Similarity 98.22
Best Local Similarity 98.22
Best Local Similarity
Conservative
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1615 GGGCTGCGGCAGGGCGGGGGAGCTC 1643

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62 GGGCTGCGGCAGGCCGGGGAGCTC 90

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HSC12B081 normalized infant brain cDNA Homo sapiens cDNA clone c-12b08, mRNA sequence.
AU121731 AAAAA Homo sapiers cDNA clone MAAWA1000851 5', mRNA
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1 (bases 1 to 292)
Auffray,C., Behar,G., Bois,P., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Sebastiani-Kabaktchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                        Eomo sapiens
bykaryota: Metazoa; Chordata: Craniata; Vertebrata: Buteleostomi;
Mammalia: Butheria; Primates: Catarrhini: Eominidae; Homo.
1 (bases 1 to 763)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enal grammics for the pass sequencing: Helix HRI human oDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
                                                                                                                                                                                                                                                                                        Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1555 AATTGCGAGGGAGAGTGAGTGGGGGCCGGGACCGCAGAGCCGAGCCGACCCTTCTCTCCC 1614
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llarity 100.0%; Pred. No. 7.5e-08;
Conservative 0; Mismatches 0; Indels
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1532-3 Fara, Kisarazu, Chiba 292-0812, Japan
177el: 81-438-52-3975
Fax: 81-438-52-3986
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/note="Vector: pME18SFL3"
205 c 260 g 158 t
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/clone_lib="MAMMA1"
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                                                                                  AU121731
AU121731.1 GI:10936966
                                                                                                                                                                                                                                                                                                                                                                  HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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(bases 1 to 69570)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome, clone RP11-1N10

Unpublished

2 (bases 1 to 69570)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Lawa, R.M., Wade, D., Oram, J.F. and Garvin, M.
Atp binding cassette transporter protein abol polypeptides
Patent: WO 0070971...A 3 28-DEC-2000;
CV THERAPEUTICS, TWO. (US)
                                                                                     1394 GGGCCCCGGCTCCACGTGCTTTCTGCTGACTGAACTACATAAACAAGGCCGGGAA 1453
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             Pred. No. 1.1e-31;
Mismatches 0;
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The zinc finger protein 202 (ZNF202) is a transcriptional repressor of AIP binding cassette transporter AI (ABCA1) and ABCG1 gene expression and a modulator of cellular lipid efflux J. Biol. Chem. 276 (15), 12427-12433 (2001)
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                                                                                                                        Porsch-Oezcueruemez,M.K.

Direct Submission
Submitted (05-4AM-2000) Porsch-Oezcueruemez M.K., Institute for Clinical Chemistry, Jaiversitiy of Regensburg, Franz-Josef-Strauss Allee 11, 93042 Regensburg, GERMANY 1.1167
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315 c 327 g 247 t
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896
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Regulation with binding cassette transporter protein abcl

Patent: WO 0078972-A 3 28-DEC-2000;

CV THERAPSUTICS, INC. (US)
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                       /map="9q22-31"
/cell_type="leukocyte"
1. .1167
/gene="ABC-1"
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/chromosome="9"
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412: gap of 844 bp in length
34268: contig of 856 bc '
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36156: contig of 852 bp
56: gap of 100 bp
37128: contig of 872 bp
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49485: contig of 834 bp
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26621: contig of 851 bp
26721: gap of 100 bp
27576: contig of 855 bp
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32368: contig of 858 bp
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"December 19, "D
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                            Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 32141, USA On Jul 13, 2000 this sequence version replaced g1:6705871. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Jow-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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872 971: gap of 100 bp
1834: contig of 863 bp in length
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cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Jan 15, 2002 this sequence version replaced gi:18121468.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT, TF., TREMBL; Wp., WORMPEP, Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
RPI1-217B7 is from the library RPCI-11.1 constructed by the group of Pleter de Jong. For further details see
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Human DNA sequence from clone RPI1-217B7 on chromosome 9, complete
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1585: gap of 100 bp 5044C: contig of 855 bp in length 5140: gap of 100 bp 51404: contig of 864 bp in length 1504: gap of 100 bp 52372: contig of §68 bp in length
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Matches 139;

E9

Dp. Ãδ 엄 ŏ

121

41526

Dib

Query Match Best Local 9

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#4249. #4273

/note="Sequence from overlapping clone RPI1-122FI0
(ACO26643). Assembly confirmed by restriction digest."
(ACO5664). Assembly confirmed by restriction digest."
92050. .92163

/note="Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."

/note="Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."

73 a 21138 c 20380 g 27526 t
VECTOR: page 3.6

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VECTOR: page 3.6

RPI1-21757 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true right end of clone RPI1-21757 is at 96717 in this sequence. The true left end of clone RPI1-122FIC is at 72980 in this sequence. The true right end of clone RPI1-122FIC is at 72980 in this sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RPOI-11.1"
3238. .3278
Anote="Sequence from AF275948 sequenced by National
Institutes of Heath, National Heart, Lung and Blood
Institute, Bethesda, MD 20892, USA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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100.0%; Pred. No. 7.3e-32;
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                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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                                                                                                                                                                                                                                                       Location/Qualifiers
1. .96717
                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RP11-217B7"
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Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 96717)

Homo sapiens

ORGANISM

human.

HIG

KEYWORDS

VERSION

DEFINITION

ACCESSION

AL359182/c

RESULT 5

Skuce,C.

AUTHORS TITLE JOURNAL

REFERENCE

Direct Submission Submitted (11-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,

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4415: 0
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5785:
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                                                                                                                                  HTG 22-APR-2000
                                                                                                                              AC012230 175064 bp DNA linear HTG 22-APR-200 Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (21-0CT-1959) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 22, 2000 this sequence version replaced gi:6454033. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                           ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 117571 bases at least 040 consensus quality: 11571 bases at least 040 consensus quality: 145749 bases at least 020 consensus quality: 160940 bases at least 020 linsert size: 185000; agarose-fp insert size: 171264; sum-of-contigs Quality coverage: 2.9 in 020 bases; agarose-fp Quality coverage: 3.2 in 020 bases; sum-of-contigs
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1 (bases 1 to 1756A;
1 Tren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-1M10
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AC012230
AC012230.3 GI:7637254
HTG; HTGS_PHASEI; HTGS_DRAFT
                                 DD 17296 GCCGAATCTATAAAGGAA 17278
121 GCCGAATCTATAAAGGAA 139
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                                                                                                                            AC012230
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VERSION
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TITLE
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JOURNAL
                                                                                         RESULT 6
AC012230
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SOURCE
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3599: gar

98001: gap of

103016: contig of 4302...

103116: gap of

109178: contig of 5015 bp in length

109278: gap of

109278: gap of

111307: contig of 6062 bp in length

8 114407: gap of

100 bp

124079: contig of 6672 bp in length

1010 bp

124179: gap of

100 bp

114179: gap of

100 bp

114179: gap of

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12253: com
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7879: con
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Homo sapiens ATP binding cassette transporter [ (ABCA1) gene, - PRE258623-
                                                                                                                                                                                 PAT 21-MAR-2001
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University of California, San Francisco, 505 Parnassus Avenue, San
Francisco, CA 94143-0130, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euticria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1167)
1 (bases 1 to 1167)
2 (bases 2 to 1167)
3 (bases 2 to 1167)
3 (bases 2 to 1167)
4 (bases 2 to 1167)
5 (bases 2 to 1167)
6 (bases 2 to 1167)
7 (bases 2 to 1167)
8 (bases 2 to 1167)
                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata: Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrinini, Hominidae, Homo.

        Qy
        61 CGGGGGGGGGGGGGGGGGGGGGGCTTTGACCGATACTAACCTCTGCGCTCGGTGCA 120

        Db
        28691 CGGGGGGGGGGGGGGGGGAGAGCACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCA 28750

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                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 183999)
Elayden, M. R., Brooks-Wilson, A. R., Pimstone, S. N. and Clee, S. M. Compositions and methods for modulating hdl cholesterol and triglyceride levels
Patent: WO 0115676-A 1 08-MAR-2001;
University of British Columbia (CA); Xeron Genetics Inc. (CA)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 183999;
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100.0%; Score 139; DB 6; Length 18

Best Local Similarity 100.0%; Pred. No. 6.8e-32;

Matches 139; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              386 others
                                                                                                                                                                                   linear
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                                                                                                                                                                                     DNA
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/db_xref="taxon:9606"
49549 a 37944 c 41170 g 54950 t
                                                                                                                                                                     183999 bp
Sequence 1 from Patent W00115676.
AX092589
AX092589.1 GI:13444647
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                         bp in length.
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/organism="Homo sapiens"
/db xref="taxon:606"
/clone="RP11-1M10"
/clone_lib="RPCI-11 Human Male BAC"
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Sequence 1 from Patent W00115676. AX092589 AX092889.1 GI:13444647	human. Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;	.N. and C choleste	triglyceride levels Park-2001; Patent: Wo Olls676-A 1 06-MAR-2001; Patent: Wo Olls676-A Columbia (CA); Xenon Genetics Inc. (CA) Location/Qualifiers	irce 1. 18339 "Homo sapiens" /organism="Homo sapiens" /db_xref="taxon:9606" NY 49549 a 37944 c 41170 g 54950 t 386 others	Natch 90.6%; Score 1387.6; DB 6; Length 183999; Soci Similarity 97.7%; Pred. No. 0; 1503; Conservative 2; Mismatches 10; Indels 23; Gaps 9;	GGCTCCACATGCACTTCCAGGGCCTGCTTGGCTCTTCTATGGGTCTGTCCTCAGTGTT 73 1117 117 117 117 1117 11	GATAGAACCACTGATGTGAGTACCTGGGCTTGAG-CGTGGCCTGGAGATCCTGTTGACTG 132	TAGCATGGAGGGGCTTGT-CAGCTGAATGTCTGTATGCAGGTGCTGGGAGTTCTGGAAT 191 	ATGATGGAGCTGGAGGTGGGAAGAGAGTAGGCTTGGGGCACTCTCTCATGCCACCTCA 251 	TICTGGCCAAAACTCAGGTCAAACTGTGAAGGTCTAAATGTGAATCTGCCCTTCAAGGT 311 :	GGCTACAAAGGTATCTTTGTCAAGGTAGGAGACCTTGTGGCCTCCACGTGCACTTCCAGG 371	GCCTGCTT-GGCCTCTTCTACGGGTCTGCTGTGTATGAAICTCCCTTCAGG 428 	GCAGATTCATATTTAGACTCTTCACAGTTTGACCTGAGTTTTGGCCAGAATAAGGTGACA 488 	TTTAGTTTGTTGGCTTGATGAATGACTTAAATATTTAGACATATGGTGTGTAGGCCTGCA 548	TICTACTACTCTTGCCTTTTTTTTGCCCCTCCAGTGTTTTGGGTAGTTTTGCTCCCCCTAC 608	9 AGCCAAAGGGAAACAGATAAGIIGGAGGICTGGAGTGGCTACATAATTTTACACGACTGC 668	9 AATTCTCTGGCTGCACTTCACAAAIGTATACAAACTAAATACAAGTCCTGTGTTTTTATC 728
DEFINITION ACCESSION VERSION	KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE	8 6	source BASE COUNT ORIGIN	Onigin Query Matc Best Loca Matches 1	Qy 16 Db 27234	Qy 74 Db 27294	Qy 133 Db 27354	Qy 192 Db 27414	Qy 252 Db 27474	Oy 312 Db 27534	Qy 372 Db 27594	QY 429 Db 27654	Qy 489 Db 27714	Oy 549 Db 27774	QY 609 Db 27833	QY 669

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                                                                              Score 1374.4;
Pred. No. 0;
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                           /organism="Homo sapiens"
/db_xref="taxon:9606"
681 c 769 c 698
Aventis Pharma S.A. (FR)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TTGAAAGGAAACAAAAGACAAAATGATTGGCGTCCTGAGGGAGATTCAGCCTAGA
                                                                                                                                                                       GCTCTCTCCCCCCAATCCCTCCCTCCGCTGAGGAAACTAACAAAGGAAAAAATG
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Pred. No. 0;
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Sequence 1 from Patent WOO183746.
AX351029
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1 (Dases I to 149034)
Santamarina-Fojo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L., Cheng,C.F., Osorio,J., Remaley,A., Yang,X.P., Haudenschid,C., Prades,C., Chimini,G., Blackmon,E., Francois,T., Duverger,N., Rubin,E.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
                                                                                                                                                                                                                                                                                                                       PRI 17-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete genomic sequence of the human ABCAl gene: analysis of the human and mouse ATP-binding cassette A promoter Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000) 20345099
2838 CCTCTGOGCTCGGTGCAGCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCGGTAA 2897
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Submitted (08-JUN-2000) Molecular Disease Branch, National
Institutes (of Heath, National Heart, Lung and Blood Institute,
Bethesda, MD 20892, USA
                                           1557 TIGCGAGCGAGTGAGTGGGGCCGGGACCGCAGACCGAGCCGAGCCGACCTTCTCTCCCGG
                                                                                           2898 TTGCGAGCGAGGTGAGTGGGCCGGGACCGCAGAGCCGAGCCGACCTTCTCTCCCGG
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Santamarina-Fojo, S., Peterson, K.M., Knapper, C.L., Freemal
Remaley, A.T., Yang, X.-P., Haudenschild, C.C., Blackmon, E.:
Francois, T.L. and Brewer, H.B. Jr.
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/organism="Homo sapiens"
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1454. .148034
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SRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFTLKIFAXLLSPVAFGFGCEYFALFE
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YFPCTKSYWFGEESDEKSHPGSNQKRISBICMEEEPTHLKLGVSIQNLVKYYRDGMKV
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DGTLPARRNRRAFGDKQSCLRPFTEDDAADPNDSDIDPESRETDLLSGMDGKGSYQVK
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GenCore version 5.1.3
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using sw model OM nucleic - nucleic search, 3, 2003, 14:33:17; Search time 92.7366 Seconds (without alignments) 7959.555 Million cell updates/sec February Run on:

US-09-596-141C-3 1643 Title: Perfect score:

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IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

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Published_Applications_NA:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

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ALIGNMENTS

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APPLICANT: Pradex Catherine
APPLICANT: Demoir, Candrine
APPLICANT: Laurent
APPLICANT: Denefic, Laurent
APPLICANT: Denefic, Patrice
APPLICANT: Remaiser, Nicolas
APPLICANT: Remaiser, Alan
APPLICANT: Ferent, Silvia
TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying
TITLE OF INVENTION: Activity and Therapeutic Uses
TITLE OF INVENTION NUMBER: US/09/846,456
CURRENT APPLICATION NUMBER: US/09/846,456
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PAICH FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 20
SOPTWARP: FLATER
                     Seguence 1, Application US/09846456
Patent No. US20020146792A1
GENERAL INFORMATION:
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Best Local Similarity 98.1
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                                                                             APPLICANT: Rosier, Marie
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TITLE OF INVENTION: Requiatory Nucleic Acid for the ABC1 Gene, Molecules Modifying TITLE OF INVENTION: Activity and Therapeutic Uses
FILE REPERENCE: 3806.0505
CORRENT APPLICATION NUMBER: US/09/846,456
PRIOR APPLICATION NUMBER: US 60/201,280
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Version 3.0
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                                                                                                                                                                                                                                        2598 GCCCGGCGGGGGGGAGGGACGCAGGCGACCCTAAGACACCTGCTGTACCCTCCAC
                                                                                                                                                                            1437 TAAACAGAGCCGGGAACGGGGGGGGGGGGGGGGGGGGGCACAGGCTTTGACCGATAGTAA
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Pred. No. 0;
0; Mismatches
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Patent No. US20020146792A1
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APPLICANT: Prades, Catherine
PPLICANT: Lemoine, Cendrine
APPLICANT: Naudin, Laurent
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Duverger, Nicclas
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Best Local Similarity 97.99
Matches 1524: Conservative
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Fojo, Silvia
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CORGANISM: Homo sapiens
US-09-846-456-3
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SEQ ID NO 3
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1465 1525 1525 1525 1525 1645	QY 1142 CGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCTTGGCTGCCGGGAACCTGG 1201 Db 2478 CGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGCGAACGTGG 2537 QY 1202 ACTAGAGAGTCTGGGGGGGGGGGGGGGGGGGGGGGGGGG	1082 GCTCTCTCCCCCAATCCCTCCGGCTGAGGAACTAACAAAGGAAAAAATTG 114 1111111111111111111111111111111111	1022 TIGAAAGGAAACAAAAGACAAAATGATTGGCCTCCTGAGGGAGAITCAGCCTAGA 108 	962 AACAAAAGCAGCCCATTACCCAGAGGACTGTCCGCCTTCCCCTCAGCCCTAGGCCT 102	902 GGSAATCICCAAGGCAGTAGGTCGCCIATCAAAAATCAAAGTCCAGGTITGIGGGGGGAA 	842 TGAAGAGAAGGAGTAGTTCCTCTCGGGTCCTCTGAGGGACCTGGGGAGCTCAGGCT 	791 IIGTTTGTTTGTTTCTTTTTTTGTTTTTTGGCCTCCTTCCT	731 AGGGGGCTGATCAAFATAAFGAAAFTPAAAGGGGCCTGGTCCCATATTGTFCTGTGTTT 790 [111111111111111111111111111111111111	671 TTCTCTGGCTGCACTTCACAAAIGTATACAAACTAAATACAAGTCCTGTGTTTTTATCAC 730 	611 CCAAAGGCAAACAGATAGTIGGAGGICIGGAGIGGCTACATAATITTACACGACTGCAA 	551 CCTACTCTTGCCTTTTTTTTGCCCTCCAGTGTTTTGGGTAGTTTTGCTCCCCTACAG [1111/11111111111111111111111111111111	491 TAGITTGTIGGCTIGATGAATGACTAAAAATATTAGACATAIGGTGTGTGGGCCTGCATI 5 	431 AGATTCATATTTAGACTCTTCACAGTTTGACCTGAGTTTTGGCCAGAATAAGGTGACATT 	372 GCCTGCTT-GGCCTCTTCTACGGGTCTGTGGGTCTCTGTATGAATCTCCCTTCAGGGC 43 (111 1 1 1 1 1 1 1 1	312 GGCTACAAAGGTATCTITGTCAAGGTAGGAGACCTTGTGGCCTCCACGTGCACTTCCAGG	252 TTCIGGCCAAAACTCAGGTCAAACTGTGAAGTCTAAAIGTGAAICTGCCCTTCAAGGT 	192 ATGATGGAGCTGGAGGGGGGGAAGAAGTAGGCTTGGGGCAGCTGTCTCATGCCAGCTGA 	

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tory Nucleic Acid for the ABCi Gene, Molecules Modifying ity and Therapeutic Uses
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                                                                                    ACCTCCCCCAACTCCCTAGATGTCCTGGCGGGCTGAACG 1376
                            ACGCAGACCGCGACCCTAAGACACCTGCTGTACCCTCCAC 1321
                                             GECCCEGCTCCACGTGCTTCTGCTGAGTGACTGACTACA 1436
AGCCCCGAGCCCAGCGCTTCCCGCGCGTCTTAGGCCGGCGG 2597
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US 60/201,280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ruben et al.
TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REPERENCE: PA127P1
CURRENT APPLICATION UNDER: US/09/86C,673
CURRENT FILING DATON UNDER: US/09/86C,673
FIOR APPLICATION data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 289
                                                                                                                                                                                                                                                                               Length 221;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA127P1
CURRENT APPLICATION NUMBER: US/09/860,670
CURRENT FILING DATE: 2001-05-21
                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                         Score 91; DB 10; I
Pred. No. 3.7e-15;
0; Mismatches 0;
       TITLE OF INVENTION: Activity and Therapeutic Uses FILE REFERENCE: 3806.0505
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                                         CURRENT APPLICATION NUMBER: US/09/846,456
CURRENT FILING DATE: 2601-05-02
PRIOR APPLICATION NUMBER: US 60/201,280
PRIOR FILING DATE: 2006-05-02
NUMBER OF SEO ID NOS: 20
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CCGGGCTGCGCAGGCCAGGCGGGGGGGCTC 91
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7 100.0%; Pre
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                                                                                                                                                                                                                                                                                         Best Local Similarity
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GENERAL INFORMATION:
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SEQ ID NO 255
LENGTH: 32190
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Best Local Simi
Matches 62;
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                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying It
TITLE OF INVENTION: Activity and Therapeutic Uses
FILE REFERENCE: 3806.0505
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TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying 1d
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CCRRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/201,280
                                                                                                            Sequence 1, Application US/09846456
Patent No. US20020146792A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09846456
Patent No. US20020146792A1
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NUMBER OF SEQ ID NOS: 20
SOTTWARE: PatentIn version 3.0
SEQ ID NO!
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Lemoine, Cendrine
Naudin, Laurent
Denefle, Patrice
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APPLICANT: Prades, Catherine
APPLICANT: Lemoine, Cendrine
APPLICANT: Naudin, Laurent
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Duverger, Nicolas
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Brewer, Bryan
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Remaley, Alan
Fojo, Silvia
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Fojo, Silvia
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APPLICANT: Prades, Cathe
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GENERAL INFORMATION:
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APPLICANT: Lillie, James
APPLICANT: Enow, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Van Huffel, Christophe
APPLICANT: Van Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REFERENCE: MRI-0168
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                     717 IGTGTTTTTATCACAGGGAGGCTGATCAATATAAATGAAATTAAAAGGGGGCTGGTCCCAT 776
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: Pall0
CURRENT APPLICATION NUBER: US/09/764,855
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 334
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 60
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                                                                                                                          204 TITGITIGITIGATION 172
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CURRENT FILING DATE: 2001-04-13
PRICA APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOFTWARE: PastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 994, Application US/09834975
Patent No. US20020110815A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                               Sequence 60, Application US/09764855
Patent No. US20020119919A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.5%;
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Best Local Similarity
Matches 51, Conserv
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US-09-834-975-994
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Publication No. US20020198362A1
CENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Annion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METEODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
FILE REFERENCE: 2077.001200
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                                                                                                     Score 43.4; DE
Pred. No. 0.49;
                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                              0; Mismatches
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PRIOR FILING BATE: 2000-08-04
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: Faster for Windows Version 3.0
SEQ ID NO 8332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/796,692
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PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
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PRIOR FILING DATE: 20C0-05-01
PRIOR APPLICATION NUMBER: 66/202,084
PRIOR PLING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR PLING DATE: 200C-05-22
PRIOR PLING DATE: 200C-07-14
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR FILING DATE: 200C-07-14
PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
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Best Local Similarity 65.67
Matches 61; Conservative
                                                                                                                                           62; Conservative
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LENGTH: 32249
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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Score 40.2; DI
Pred. No. 0.5;
0; Mismatches
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        Application US/39878574
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O
                                                  APPLICANT: Byrum, Joseph R. APPLICANT: La Rosa, Thomas J. APPLICANT: Thompson, Michael D.
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ilarity 62.1%;
Conservative (
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                     US20020110548A1
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Best Local Similarity
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Best Local Similarity
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US-10-008-118A-19
                       Patent No. US2002311
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure
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US-10-008-118A-19/c
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.9
SEQ ID NOS 9372
LENGTH: 12718
                                                                                                                                              . TITLE OF INVENTED ACIDS, Proteins, and Antibodies TITLE REPERENCE: PIL4
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-27
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Rosen et al.
IITLE OF INVENTOR: Nucleic Acids, Froteins, and Antibodies
FILE REFERENCE: PC005
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                                 45;
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60.2%; Pred. No. 1.3;
tive 0; Mismatches 45;
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                                                                                                                                           Sequence 14, Application US/09764870 Patent No. US20020642386A1
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Best Local Similarity 60.2
Matches 68; Conservative
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ORGANISM: Homo sapiens
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GRGANISM: Homo sapiens
US-09-764-877-3972
                                                                                                             RESULT 11
US-09-764-870-14/C
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US-09-878-574-4299
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RESULT 15

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TITLE OF INVENTION: Notice Acid Molecules and Other Molecules Associated with TITLE OF INVENTION: Plants
FILE REPRENCE: 38-21(15401)8
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR PRILING DATE: 1939-06-14
NUMBER OF SEQ ID NOS: 15775
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TITLE OF INVENTION: Plant MY3-Related Transcription Factors
FILE REFERENCE: Bal28 USDIV
CURRENT APPLICATION NUMBER: US/10/008,118A
CURRENT APPLICATION NUMBER: US/10/12-05
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 50
SOFWARE: Microsoft Office 97
SEQ ID NO 19
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Pred. Nc. 0.27;
                                                                                                                                                                                                                                                                                                                     LOCATION: (1)...(545)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3028-013-Q1-B1-H1
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US-09-443-704-19/c

Sequence 19, Application US/09443704

Fatent No. US/0000066120a1

GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Liz, Zhan-Bin
APPLICANT: Affil, Jan-Bin
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Meng, Zude
TITLE REFERENCE: BB1280 CE NA
CURRENT APPLICATION WIMBER: US/09/443,704

CURRENT FILING DATE: 1999-1119

EARLIER APPLICATION NUMBER: 60/109,294

EARLIER PILICATION NUMBER: 60/109,294

EARLIER PRICO DATE: 50

SOFTWARE: Microsoft Office 97

SEQ ID NO 19

LENGTH: 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : TYPE: DNA
; ORGANISM: Zea mays
US-69-443-704-19
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Search completed: February 3, 2003, 16:23:44 Job time : 299.737 secs

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NO.

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COUNTRY: USA
CONFORTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-COS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2989
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US-08-232-463-14
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Matches
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14, Appl
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Sequence 36, Appl
Sequence 1, Appli
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20, Appl
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                                                             ; Search time 77.1143 Seconds
(Without alignments)
6534.066 Million cell updates/sec
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                                                                                                                             Description
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2: /cgn2_6/ptcdata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptcdata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptcdata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptcdata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptcdata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-493-533-4
US-08-493-533-4
US-09-283-471A-4
US-09-283-471A-36
PCT-US91-06532-1
US-09-149-476-24
US-09-149-476-24
US-09-149-476-24
US-08-829-838-1
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US-08-804-227C-1
US-08-960-022-17
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                                                                2003, 12:56:40
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                                           nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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                                                                                                         US-09-596-141C-3
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Match Length DB
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Sequence 1, Appli
Sequence 3, Appli
Sequence 9, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 11, Appli
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Sequence 4, Appli
Sequence 67, Appl
Sequence 4, Appli
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                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MCEVER, RODGER P. TITLE OF INFLAMMATORY RESPONSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42;
                                                                                                                                                                                                                                                                                                                                                                                                  BY ADMINISTRATION OF GMP-140 OR ANTIBODY TO GMP-140 NUMBER OF SEQUENCES: 32
  US-08-776-844-1
US-09-247-3738-33
US-08-072-574-7
US-08-072-574-9
US-08-072-574-9
US-08-061-376-4
US-08-104-073-2
US-08-104-073-2
US-08-104-073-2
US-08-104-13-13-14-10
US-09-133-745-10
US-09-133-840A-1
US-09-133-840A-1
US-08-361-4678-1
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APPLICANT: SCHRIFTINGER, F.
APPLICANT: FALKNER, F.
ITLE OF INVENTION: RECOMBINANT FOMLDOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.6%; Score 42.8; D
61.8%; Pred. No. 0.03
ive 0; Mismatches
                                                                                                                                                                                                                                                                                        ALIGNMENTS
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APPLICATION NUMBER: US/07/320,408
FILING DATE: 08-MAR-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 14, Application US/08232463; Patent No. 5670367; GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
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Les 68; Conserv
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COMPUTER READABLE FORM:
                                                                                                    FILING DATE: 07 CLASSIFICATION:
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STREET: 6300
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2.5%; Score 40.5; DB 1;
3est Locai Similarity 4.2%; Pred. No. 0.25;
Matches 13; Conservative 171; Mismatches 125;
                                                                                                                                                                             30472/214 IMMU
                                                                                             BP 91 114 300.6
                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
APPLICATION NUMBER: US/08/232,463
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RY: United States of America
60506-6402
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Patent No. 6172047
GENERAL INFORMATION:
APPLICANT: Roizman, Bergard
APPLICANT: Chou, Joany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Method for
TITLE OF INVENTION: Diseases
                                                                                                                                                           29,768
                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 30
TELECOMEOUNICATION:
TELEPHONE: (703)836-930
TELEPHONE: (703)83-4109
                                                                                          APPLICATION NUMBER: EP 9
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                   LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                          NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                    TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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               FILING DATE:
CLASSIFICATION: 435
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STREET: bocc
Trav: Chicago
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                                                                              FILING DATE:
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STATE: I.
COUNTRY:
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1171 CCACTGGTGCCCTTGGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGCGCAGCCCCGAGC 1230
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00 Sears Tower, 233 South Wacker Drive
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/483,533
FILING DATE: 07-MAR-95
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49.2%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                       28097/32742
                                                                                                                                                                                                                FILING DATE: 111-AFM 52
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/861,233
FILING DAIE: 31-MAR-92
ATORNEY AGENT INFORMATION:
NAME: 2eller, James P.
REGISTRATION NUMBER: 28,491
REGISTRATION NUMBER: 28097/3
TELEPHONE: 212/474-6300
TELEFAX: 312/474-6448
TELEFAX: 312/474-6448
TELERAX: 35-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISICS:
COMMENT OF SEQ ID NO: 4:
SEQUENCE CHARACTERISICS:
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STATE: Illinois
COUNTRY: United States of America
ZIP: 6060-6402
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Patent No. 6340673
GENERAL INFORMATION:
Roizman, Bernard
APPLICANT: Roizman, Jernard
APPLICANT: Chou, Joany
TITLE OF INVENTION: Method For Tr
                                                                                                                                                                                           APPLICATION NUMBER: 08/419,853
FILING DATE: 11-APR-95
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MOLECULE TYPE: DNA (genomic)
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nucleic acid
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Matches 131; Conservative
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Tue Feb

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FILING DATE: 31-MAR-92 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                            NAME: Zeller, James P. REGISTRATION NUMBER: 28 REFERENCE/DOCKET NUMBER:
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Best Local Similarity 49.2
Matches 131; Conservative
                                                                                                                                                                      FILING DAIE: 07-MAR-95
CLASSIETCATION: 514
PRIOR APPLICATION DATA
APPLICATION NUMBER: 08
FILING DAIE: 11-APR-95
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APPLICATION NUMBER: (
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                                                      COMPUTER READABLE FORM:
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       Illinois
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                     COUNTRY:
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STREET: 6300 Sears Tower, 233 South Wacker Drive
                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Method for Treating TITLE OF INVENTION: Diseases
                                                                                                                                                                                                                                                                                                                                           27373/32742A
                                                                                   US/09/283,471A
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                                   PC-DOS/MS-DOS
                                                                                                                                                               FILING DATE: 31-MAR-1992
PRIOR APPLICATION DAIA:
APPLICATION NUMBER: 09/419,853
                                                                                                                                                      07/861,233
                                                                                                                                                                                                                                                      08/483,533
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Patent No. 6172047
GENERAL INFORMATION:
1: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                     NAME: Zeller, James P.
REGISTRATION NUMBER: 28,491
                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 77
TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Roizman, Bernard APPLICANT: Chou, Joany
                                                                                                                                                                                                                  FILING DATE: 11-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/48
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                               04-APR-1999
                                                                                                                                                                                                                                                                                                                                                                          : 312/474-63C0
312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTE: 595 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 49.2
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER: (
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                                                                                   APPLICATION NUMBER:
                 COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                 FILING DATE: 0. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chicago
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1171 CCACTGGTGCCCTTGGCTGCCGGGAACGTGGAGTAGAGAGTCTGCGGCGCAGCCCGGAGC 1230
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APPLICANT: Chou, Joany
TITLE OF INVENTION: Method For Ireating Tumorigenic Diseases
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 1327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Pred. No. 0.33;
0; Mismatches 132;
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YY: United States of America
60606-6402
                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,533
FILING DATE: 07-MAR-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1408 CGIGCTTTCTGCTGAGTGACTGAACT 1433
                                                                                                    MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS OPTIMARE: Patentin Release
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: C8/419,853
11-APR-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07/861,233
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TELEPHONE: 312/474-6300
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INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHRACTERISTICS:
STANDARD E STANDARD STANDARD
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US-08-483-533-36
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1171 CCACTGGTGCCCTTGGCTGCCGGGAACGTGGAGTTTGAGGGTCTGCGGCCCAGCCCCGAGC 1230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US91/06532
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.4%; Score 38.8; DB 5; Best Local Similarity 49.2%; Pred. No. 0.33; Matches 131; Conservative 0; Mismatches 132;
                      Suite 2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE FAPERENCE: P2002P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-39-08
BARLIER APPLICATION NUMBER: PCT/US98/34493
EARLIER FILING DATE: 1998-33-06
EARLIER FILING DATE: 1997-73-07
EARLIER FILING DATE: 1997-73-07
EARLIER APPLICATION NUMBER: 60/346,333
EARLIER APPLICATION NUMBER: 60/346,333
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    ADDRESSEE: Bicknell
STREET: Two First National Plaza
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                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DGS/MS-DGS
                                                                                                                                                                                                                                                                                                                               30,060
                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                               IELERA: 312/994-9740
TELERA: 25-3856
INFORMATION FOR SEQ ID NC: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,0
                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
      Abbac
STREET: 1*C
CITY: Chicago
'-me: Illinois
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Pred. No. 0.33;
0; Mismatches 132; Indels
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                                                                                                                        SCFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/283.471A
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Illinois
: United States of America
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Sequence 1, Application PC/TJS9106532
GENERAL INFORMATION:
                                                                                                                PC-DOS/MS-DOS
                                                                                                                                                                                                                                                  07/861,233
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                                                                        Eloppy disk
IEM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NORBER: 28,491
REFERENDE/DOCKET NUMBER: 27:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELETAX: 312,
TELETAX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1327 base pairs
"VPE: nucleic acid
"VPE: nucleic acid
                                                                                                                                                                                                                                                              FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/419
FILING DATE: 11-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/483,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLEÇULE TYPE: DNA (genomic)
US-09-283-471A-36
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Zeller, James P.
                                                                                                                                                                                    FILING DAIE: 04-APR-1
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
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CORRESPONDENCE ADDRESS:
                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                OPERATING SYSTEM:
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TITLE OF INVENTION:
                                  60636-6402
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                                                                                            COMPUTER:
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EARLIER APPLICATION NUMBER: 60/046,526
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,312
APPLICATION DATE: 1997-04-11
APPLICATION NUMBER: 60/043,313 APPLICATION NUMBER: 60/043,314 FILING DAIE: 1997-04-11 APPLICATION NUMBER: 60/043,569 FILING DATE: 1997-04-11
APPLICATION UNBER: 60/043,311
BILING DATE: 1997-04-12
APPLICATION NUMBER: 60/043,671 APPLICATION NUMBER: 60/043,669 FILING DATE: 1997-04-11 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,568 60/043,674 APPLICATION NUMBER: 60/047,601 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,580 1997-05-2 1997-04-1 1997-04-1 997-04-FILING DAIE: 1997-0. APPLICATION NUMBER: FILING DATE: 1997-0. DATE: FILING DATE: FILING BARLIER
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1997-08-22 (IMPER: 60/056,892) APPLICATION NUMBER: 60/047,589 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,586 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,593 FILING DATE: 1997-05-23 60/056,845 60/057,761 60/047,595 60/047,599 60/047,588 60/047,585 60/047,590 60/047,594 APPLICATION NUMBER: 60/056,872 FILING DATE: 1997-08-22 ING DATE: 1997-08-22 LICATION NUMBER: 60/056,894 APPLICATION NUMBER: 60/056,910 APPLICATION NUMBER: 60/056,889 FILING DATE: 1997-08-22 60/056,879 EARLIER APPLICATION NUMBER: 60/056,880 60/056,911 60/056,636 60/056,874 60/056,854 60/056,631 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,315 APPLICATION NUMBER: 60/056,886 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,877 FILING DATE: 1997-08-22 60/056,630 60/056,878 60/056,652 60/056,882 60/056,637 60/056,903 60/056,888 60/056,893 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/C EARLIER APPLICATION NUMBER: 60/C EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 EARLIER FILING DATE: 1997-08-22 -05-23 NG DATE: 1997-08-22 ICATION NUMBER: 60/ 1997-08-22 1997-08-22 FILLING DATE: 1997-08-22 APPLICATION NUMBER: 60/ FITTING PAGE -05 - 231997-05-23 APPLICATION NUMBER: 60/ FILING DAIE: 1997-08-22 1997-08-22 LICATION NUMBER: 60/ ING DATE: 1997-05-23 1997-05-23 1997-08-22 1997-08-22 1997-08-23 1997-08-22 -08-22 1997-08-2 .997-08-2 1997-08-2 ICATION NUMBER: 60. 1997-05-R APPLICATION NUMBER: 6 R FILING DATE: 1997-08-R APPLICATION NUMBER: 6 R FILING DATE: 1997-08-APPLICATION NUMBER: FILING DATE: 1997-05 APPLICATION NUMBER: APPLICATION NUMBER: LICATION NUMBER: LICATION NUMBER: FILING DATE: 1997-08 APPLICATION NUMBER: LICATION NUMBER: ICATION NUMBER: APPLICATION NUMBER: CATION NUMBER: APPLICATION NUMBER: TON NUMBER: APPLICATION NUMBER: ILING DATE: FILING DATE: FILING DATE: FILING DATE: DATE: FILING DATE: FILING DATE: LING DATE: FILING DATE: DAIE: FILING DATE: DATE: ING FILING FILING FILING EARLIER APPLI EARLIER FILIN EARLIER APPLI EARLIER F EARLIER F EARLIER Z EARLIER Z EARLIER I EARLIER I EARLIER I EARLIER EARLIER ZEARLIER Z EARLIER / EARLIER | EARLIER / EARLIER EARLIER EARLIER EARLIER EARLIER / EARLIER 1 EARLIER A EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER PARLIER PARLIER PARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER BARLIER EARLIER EARLIER EARLIER EARLIER

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APPLICANT: Rosen et al.
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CURRENT APPLICATION NUMBER: US/09/149,476
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EARLIER APPLICATION NUMBER: PCT/US98/04493
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FILING DATE: 1997-10-02
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APPLICATION NUMBER: 60/047,501
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US-09-149-476-24/c
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,637
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,903
FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,888 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,879 FILING DATE: 1997-08-22 APPLICATION WUMBER: 60/056,894 FLING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,911 APPLICATION NUMBER: 60/056,636 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,874 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,599 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,586 JMBER: 50/047,590 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,614 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,578 EARLIER APPLICATION NUMBER: 60/056,886 FILING DATE: 1997-08-22 APPLICATION UNDBER: 60/056,630 ALLING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,878 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,910 1997-08-22 UMBER: 60/056,631 APPLICATION NUMBER: 60/056,845 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/057,761 60/047,595 60/047,588 60/047,589 EARLIER FILING DATE: 1997-04-11 EARLIER APPLICATION NUMBER: 60/048,974 EARLIER FILING DATE: 1997-06-06 1997-08-22 JMBER: 60/056,872 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,882 50/056,880 60/056,864 APPLICATION NUMBER: 60/056,892 APPLICATION NUMBER: 60/047,585 60/047,594 60/026,889 60/056,893 60/056,662 EARLIER APPLICATION NUMBER: 60/043,315 60/056,877 1997-05-23 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/ 1997-05-23 1997-05-23 1997-05-23 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/ 1997-08-22 1997-08-2 1997-08-22 1997-08-2 1997-08-2 APPLICATION NUMBER: FILING DATE: 1997-05 FILING DATE: 1997-05 APPLICATION NUMBER: FILING DATE: 1997-08 APPLICATION NUMBER: FILING DATE: 1997-08 APPLICATION NUMBER: FILING DATE: 1997-0: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: FILING DATE: DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING EARLIER PEARLIER PEARLIER EARLIER SARLIER SARLIER EARLIER EARLIER BARLIER / EARLIER | EARLIER / EARLIER PARLIER PARLIE EARLIER BARLIER
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Gaps 0; Length 2323; 29; Indels TITLE OF INVENTION: Proapoptotic Peptides, Dependence TITLE OF INVENTION: Polypeptides and Methods of Use NUMBER OF SEQUENCES: 72 CORRESPONDENCE ADDRESS: ADDRESSEE: Campbell & Flores LLP STREET: 4370 La Jolla Village Drive, Suite 700 Patentin Release #1.0, Version #1.25 DB 4; Score 38.6; DB Pred. No. 0.5; 0; Mismatches EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,867
EARLIER FILING DATE: 1997-08-22 UMBER: 60/056,908 1997-08-22 UMBER: 60/056,884 1997-08-22 UMBER: 60/057,669 CMBER: 60/056,664 NUMBER: 50/061,060 1997-10-02 60/057,650 60/049,610 60/043,576 EARLIER APPLICATION NUMBER: 60/043,670 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/056,632 60/056,876 606'950/09 60/056,875 60/048,964 60/047,501 60/056,881 2222 AATTTATTAAAATAAGAACAAGCAT 2198 COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 836 AATTTAIGAAGAGAAGCAGTAAGAI 860 US-09-041-886-18; Sequence 18, Application US/09041886; Patent No. 6235872 1997-09-05 1997-06-06 APPLICATION NUMBER: 602 FILING DATE: 0-50-1997-06-13 1997-08-22 2.3%; 1997-05-23 1997-08-2 Abb...
STREET: 43/c
CITY: San Diego
STATE: California
...wmpY: United States EARLIER APPLICATION NUMBER: 6(
EARLIER FILING DATE: 1997-08-2
EARLIER APPLICATION NUMBER: 6(
EARLIER FILING DATE: 1997-09-08
EARLIER FILING DATE: 1997-06-1 1997-04-ARLIER APPLICATION NUMBER: 6
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US-08-829-839-1
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APPLICANT: Locatscher, Marcel
APPLICANT: Moser, Bernhard
TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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STREET: Two Militia Drive
CITY: Lexington
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Paterin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,838
                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
REFERENCE/OCKET NUMBER: P-LJ 2626
TELEPENOR: (619) 535-9001
TELEPENX: (619) 535-9001
TELEPENX: (619) 535-9001
TELEPENX: (619) 535-8949
INFORMATION FOR SEQ ID NG: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 4481 base pairs
TYPE: INCleic acid.
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ATTORNEY/AGENT INFORMATION:
NAME: BROCK BSQ., David E:
REGISTRATION NUMBER: 22,592
RETERENCE/DOCKET NUMBER: TK196-01
TELECHONOLICATION INFORMATION:
TELECHONE: (617) 861-6240
TELEFAX: (617) 861-9540
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/041,886
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; Sequence 1, Application US/08709838
; Patent No. 5140064
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                                                               CLASSIFICATION:
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US-09-041-886-18
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APPLICANT: Loetscher, Marcel
APPLICANT: Moser, Bernhard
APPLICANT: Moin, Shixin
APPLICANT: Mackay, Charles R.
APPLICANT: Mackay, Charles R.
TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
TITLE OF INVENTION: ANTIBODIES, NJCLEIC ACIDS, AND METHODS OF USE THEREFOR
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Two Militia Drive
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                                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                       Query Match 2.3%; Score 38.2; DB Best Local Similarity 59.8%; Pred. No. 0.55; Matches 54; Conservative 0; Mismatches
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FILING DATE: 31-MAR-1997
CLASSIPTICATION: 435
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/709,838
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08829839
Patent No. 6184358
GENERAL INFORMATION:
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REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TKI
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INFORMATION FOR SEQ ID NO: 1
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1670 base pairs
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EDNESS: double
                                                           TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
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OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
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OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
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LOCATION: 72771...72817
OTHER INFORMATION: Polymorphic fragment 5-124-273 SEQ
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OTHER INFORMATION: polymorphic fragment 5-124-273
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 5-133-375
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90819..90865
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LOCATION: 90819..90855
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LOCATION: 88050..88096
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LOCATION: 88050..88096
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NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION: 5
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OTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
                          NAME/KEY: allele
LOCATION: 108106
OTHER INFORMATION:
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NAME/XEY: allele
                                                                                              LOCATION: 108149 OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: allele
Tocamton: 146328
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LOCATION: 150329
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LOCATION: 108308
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LOCATION: 134362
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TIILE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AND POLYMCRPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
                              0
                                                                                1562 ICTITIATITITATGECTAAAATCCTGCTTAAAACTITICAATAAACAAGATGGECAGGA 1621
                                                        714 ICCTGTGTTTTTATCACAGGGAGGCTGATCAATATAATGAAATTAAAAGGGGGCTGGTCC 773
                             Gaps
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  Score 38.2; DB 4; Length 1670; Pred. No. 6.55; ); Mismatches 43; Indels 0
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                                                                                                                                                                                                                                                                                  FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
                                                                                                                                                                                         US-09-345-882-1/c; Sequence 1, Application US/09345882; Patent No. 6399373
                              0;
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     2.3%;
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     Query Match 2.3°
Best Local Similarity 59.8°
Matches 64; Conservative
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 103806
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LOCATION: 106940
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LOCATION: 72794
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LOCATION: 90842
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                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08018577C
Patent No. 568601
GENERAL INFORMATION:
APPLICANT Weber, Peter C.
TITLE OF INVENTION: BNA Sequences Encoding Mutant Antiviral TITLE OF INVENTION: Regulatory Proteins
NUMBER OF SEQUENCE: 6
CORRESPONDENCE ADDRESS:
ADDRESSE:
The Pennsylvania State University
STREET: 113 Technology Center
CITY: University Park
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MEDIUM TYPE DISKette, 3.50 inch, 720 Kb storage CCMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS 6.22
                                                                                                                                                        TTTTTTTGTTTTTGTGGCCCCCCTCCTCTCAATTTAIGAAG 846
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Microsoft Word for Windows 6.0
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APPLICATION NUMBER: US/08/018,977C
FILING DATE: 18-FEB-1993
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TELECOMMUNICATION INFORMATION:
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TELEFAX: (814) 865-3591
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 05-JUL-1991 ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: genomic DNA
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
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ZIP: 16802-7000
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US-08-018-977C-4/C
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LOCATICN: 108127...1081.77
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
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OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
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                                          OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
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LOCATICN: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ
                                                                                                                                                                                                                                                                           SEQ
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OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ
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OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ
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                                                                                                                      OTHER INFORMATION: polymorphic fragment 99-1442-224
                                                                                                                                                                                                                                  NAME/KEY: allele
LOCATION: 97130..37177
OTEER INFORMATION: polymorphic fragment 5-129-144
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OTHER INFORMATION: polymorphic fragment 5-129-144
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LOCATION: 108084..108130
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FEATURE:
NAME/KEY: allele
TTAN: 99075.99121
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LOCATION: 99094..99140
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93690..93736
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97099..97145
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TION: 99075..99121
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LOCATION: 108127.
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NAME/KEY: allele
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LOCATION: 103783.
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NAME/KEY: allele
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NAME/KEY: alleie
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Indels

77;

Query Match 2.3%; Score 37.8; DB 4; Best Local Similarity 52.2%; Pred. No. 8.4; Matches 84; Conservative 0; Mismatches 77;

Length 152450;

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Query Match 2.3%; Score 37.4; DB 1, Length 767; Best Local Similarity 62.1%; Pred. No. 0.51; Matches 59; Conservative 0; Mismatches 36; Indels (
                         Sequence 1, Application CS/08184604
Patent No. 5389537
GENERAL INFORMATION:
APPLICANT: delCardayre, Stephen B.
APPLICANT: Raines, Ronald T.
TITLE OF INVENTION: Nuclease having airered specificity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles and Brady
SIREET: 1 South Pinckney Street, PC BOX 2113
COITY, Madison
                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 53701-2113
COMPUTER READBLE FORM:
MEDIUM TYPE: 5-OPPY disk
COMPUTER: 1BM PC COMPATIONE
SPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
A-PLICATION NUMBER: US/08/184,604
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INPORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 96-296-9266-2
TELEPHONE: 608-251-500
TELEPHONE: 608-251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 767 base pairs
TYPE: nucleic acid
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US-08-184-604-1
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RESULT 15
US-08-184-604-1/C
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CITY: Ma
STATE: W
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ó Gaps

QQ QY

Search completed: February 3, 2003, 16:19:27 Job time : 319.114 secs

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February 3, 2003, 12:46:48 ; Search time 418.41 Seconds (without alignments) 8245.650 Million cell updates/sec
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/SIDS2/gcddata/geneseq/geneseqn.embl/NA1981.DAT:*
/SIDS2/gcddata/geneseq/geneseqn.embl/NA1981.DAT:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2185239 seqs, 1125999159 residues
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Maximum DB seq length: 2000000000
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					SUMMARIES	
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(4)	1387.6	90.6	90.6 183999	22	AAF92831	Human ABC1 genomic
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Garvin M;

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(CVIH-) CV THERAPEUTICS INC.

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The present sequence represents the 5' flanking region of the human denosine triphosphate (ATP) binding cassette protein (ABC) I gene. ABCI resides in cell membranes and utilises ATP hydrolysis to transport a wide protein in the apolipoprotein-mediated mobilisation of intracellular protein in the apolipoprotein-mediated mobilisation of intracellular choiserrol stores. ABCI is defective in Tanglar disease, a genetic choiserrol stores. ABCI is defective in Tanglar disease, a genetic disorder characterised by abnormal HDL-folesterol metabolism. The ABCI gene is localised to chromosome 9422-9431. The ABCI genes and proteins are useful for developing pharmaceutical agents for the treatment of neart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and cother disorders associated with hypercholesterolemia.
                                         useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis
                         Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide.
                                                                                                                                                                       Claim 1; Page 143-144; 215pp; English.
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Sequence 1643 BP; 370 A; 413 C; 457 G; 403 T; 0 other;

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       DB 22; Length 1643;
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                     Pred. No. 0; Mismatches
100.0%; Score 1532;
ilarity 100.0%; Pred. No. 0;
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                           TTTTTATCACAGGGAGGCTGATCAATATAATCAAATTAAAAGGGGGCTGGTCCCATATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1501 TGGGCTGGTGCAGCGAATCTATAAAAGGAA
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The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (ATP) binding cassette protein (AEC) 1 gene. ABC1 resides in cell membraces and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrace. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangler disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                         Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
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apolipoprotein-mediated mobilisation; cholesterol; Tangler chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
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99US-0153872.
99US-0166573.
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19-NOV-1999;
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                                         GCACTTCCAGGGCCTGCTTGGCCTCTTCTACGGGTCTGTCCTGAGTCTTCTATGAATCTC
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COGITTAAGGGGGGGGGCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAA 1440
                                      selected
                                                                                                                                                                                                                                                                            High density lipoprotein-cholesterol, HDL-C; cardiovascular; ABCl; ds
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                          CAGAGGCCGGGAACGGGGGGGGGGGGGAGGAGCACAGGCTTTGACCGATAGTAACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) lavel, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcriptional activity or ABC1 expression or activity.
The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition lower than normal HDL colesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
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90.6%; Score 1387.6;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1503; Conservative 2; Mismatches
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2000US-0213958.
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23-JUN-2000;
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27354 TAGCATGGAGGGGCTTGTGCAGCTGAATGTCTGYATGCAGGTGGAGTTCTGGAAT
                                                                                     27594 GCCTGCTTGGGCCTCTTCTACGGGTCTGTCCTGAGTCTTCTATGNAATCTGTCCTTCAGG
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                                                           ATGATGGAGCTGGAGGTGGGAAGAAGTAGGCTTGGGGCAGCTCTCTCATGCCACCTCA
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"LMO2-COM/MYOD/deltaEF1/E47"
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|189..1209
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/bound_moiety= "PPAR/NKX2.5/PPAR"
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bound_moiety= "DeltaEF1/LYF1/IX2'
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/bound_moiety= "HFH2/SRX/EVI1"
803..812
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|597..1607
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                           /*tag= 1
/bound_moiety= "NFY/CAAT"
708..715
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/bound_moiety= "LKX2.5"
608..620
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/bound_moiety= "NKX2.5"
1076..1089
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/bound_moiety= "M2F1"
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498..1514
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/bound_moiety= "
1685..1698
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/bound_moiety= "
1978..1985
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723..730
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1840..1850
/*tag= af
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/bound_moiety= "
1942..1956
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1632..1637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, ATP-binding cassette 1; ABC1 gene regulation; atherosclerosis; cholesterol metabolism; hypercholesterolaemia; antisense therapy; ds.
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/bound_moiety= "LMO2COM/MYOD/DeltaEF1"
549..556
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97..107
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/bound_moiety= "S8/NKX2.5"
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590..596
/*tag= k
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/bound_moiety= "DeltaEF1"
|110..125
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/bound_molety= "LYF1"
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/bound_moiety= "IK2"
il2..420
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/bound_moiety= "S8"
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/bound_moiety= "
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"GAIA" "SOX5" "SYR/HFH/HNF3beta" "KZF1" "IK2/NFXappaB/CREL"	"LMO2COM/GATA" "MZF1/SRY" "PPAR" "PPAR" "AZF1"	"HNP3beta/SRY/EVII" "MZF1" "AP4" "SCAT"	"STAT/PPAR" "PPAR" "AP2" "MZE1"	"RREB1" "MZF1/CMYB" "SP1/GC" "JSF/WMYC/ARNT"
20512059 /*tbg= ak /bound_moiety= " 1042:11 /*tag= al /bound_moiety= " 1142152 /*tag= am /bound_moiety= " 2221228 /*tag= an /bound_moiety= " 2231224 2231224 /*tag= ao /bound_moiety= " 2231224 2231224 2231224 22392272	/*tag- ap /*tag- ap 2289.7306 /*tag- aq /*tag- ad /*tag- ar /*tag-	2361238¢ /*teg= au /bound_moiety= 24262433 /*teg= av /bound_moiety= 2442249 /*tag= av /*ta	/bound_moiety= 256.2541 /*tag=2541 /*tag=2600 /*tag=26000 /*tag=26000000000000000000000000000000000000	/*tag= De //ound_molety= 2680.2698 /*tag= bf /*tag= bg //tag= bg //tag= bg //tag= bh //tag= bh //tag= bh //tag= bh //tag= bh //tag= bh //tag= bh //tag= bh
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Brewer 3, Duverger N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 3231;
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                                              Isolated nucleic acid useful for modifying the ATP-binding (ABC1) and screening for candidate modulatory compounds or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.78;
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Matches 1504; Conservative
2002-154404/20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human large ATP-binding cassette transporter 1(hABC1) promoter sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1081
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                                                                                                                                      1021
                                                                                                                                                                                                              1082 GCTCTCTCTCCCCCAATCCCTCCCTCCGGCTGAGGAAACTAACAAAGGAAAAAAATTG 1141
                                                                                                                                                                                                                       2418 GCTCTCTCCCCCCATCCCTCCCTCCGCTGAGGAAACTAACAAGGAAAAAATIG 2477
                                                                                                                                                                                                                                                                                                                            GCCCGGGGGGGAAGGGGACGCAGACCGCGGACCCTAAGACACCTGCTGTACCCTCCAC 1321
                                                                                                                                                                                                                                                                                                2538 ACTAGAGAGTCTGGGGGGGAGCCCGAGGCCAGGGTTTCCCGGGGGTCTTAGGCGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                              TIGAAAGGAAACAAAAGACAAGACAAAATGATIGGCGTCCIGAGGGAGATICAGCCTAGA
                                                                                                                                                                                                                                                          2478 CGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGTG
                                                                                                                                                                                                                                                                                                                                      -----CCCCACCCACCCACCTCCCCCCAACTCCCTAGATGTGTCGTGGGCGGCTGAACG
                                                                                                                                                                                                                                                                                                                                                                          ACTAGAGAGTCTGCGGCGCAGCCCCGAGCCCAGCGCTTCCCGGCGCGTCTTAGGCCGGCGG
                                    2238 GGGAATCTCCAAGGCAGTAGGTCGCCTATCAAAATCCAAGGTTGTGGGGGGAA
                                                                                                                                                2358 TIGAAAGGAAACAAAAGACAAAGATIGGCGTCCTGAGGAGATTCAGCTAGA
                                                                                                                                                                                                                                                    1142 CGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGTGG
2178 TGAAGAAGCAGTAAGATGTTCCTCTCGGGTCCTCTGAGGGACCTGGGGAGCTCAGGCT
                                                                                                                                       962 AACAAAAGCAGCCCATTACCCAGAGGACTGTCCGCCTTCCCCTCACCCCAGCCTAGGCCT
                           -TITCTITGTTTCTTTTTTTTTTTTGTGGCCTCCTTCCTCTCAATTA
                                                               TGAAGAAGCAGTAACATGTTCCTCTCGGGTCCTCTGAGGGACCTGGGGAGCTCAGGCT
                                                                                                   GGGAATCTCCAAGGCAGTAGGTCGCCTATCAAAATCAAAGTCCAGGTTTGTGGGGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTCTGCGCTCGGTGCAGCCGAATCTAIAAAAGGAA 1532
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The invention relates to an isolated human large ATP-binding cassette transporter 1 (ABC1) promoter capable of directing transcription of transporter 1 (ABC1) promoter capable of directing transcription of heterologous coding sequence positioned downstream to it. The hABC1 promoter is useful for expressing foreign DNA in a host cell, by introducing into the host cell a gene transfer vector comprising the promoter operably linked to a foreign DNA encoding a desired polypeptide or RNA, where the foreign DNA is expressed. The gene transfer can be introduced into the host cell by adenovirus infection, liposome mediated transfer topical application to the cell or microhisetion. The gene further involves introducing into the cell a gene transfer vector comprising a nucleic acid segment encoding a transactivator protein capable of upregulating the ABC1 promoter, or contacting the cell with the transactivator protein. With attensactivator protein, or an agonist of the transactivator protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                                                                                                                     Novel isolated human large ATP-binding cassette transporter 1 promoter capable of directing transcription of heterologous coding sequence positioned downstream to it, useful for expressing foreign DNA in host cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCTGAGITTTGGCCCAGAAIAAGGTGACATTIAGTTTGTTGGCTTGATGGATGAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAGTGGCTACATATTTACACGACTGCAATTCTCTGGCTGCACTTCACAAATGTATAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.6%; Score 1035.4; DB 24; Length 1197; 99.6%; Pred. No. 2e-275; Live 0; Mismatches 1; Indeis 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1197 BP; 284 A; 314 C; 328 G; 271 T; 0 other;
                                                                                                                 COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 3; 68pp; English
27-APR-2001; 2001WO-US13654.
                                                        28-APR-2000; 2000US-0560372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 99.6
Matches 1069; Conservative
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                                                                                                                 (UYCC ) UNIV
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"LMO2-COM/MYOD/deltaEF1/E47"
                                                                     "LMC2COM/MYOD/DeltaEF1"
                                                                                                                                                                                                                                                                                                                                                             "LXRalpha/deltaEF1"
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/bound_moiety= "DeltaE?1/LYF1/IK2"
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                                                                                                                                                                                                                                                       "HFHZ/SRY/EVIl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "ZID/deltaEF1"
                                                                                                                                                                                                                                                                                "CREBP1/VBP"
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/bound_moiety= "NFY/CAAT"
708..715
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/bound_moiety= "LKX2.5"
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/bound_moiety= "LYF1"
558..568
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/bound_moiety= "MZF1"
723..730
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/bound_moiety= "MZF1"
771..785
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/bound_moiety= "GATA"
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/bound_moiety= "LYF1"
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399..410
/*tag= f
/bound_molety= "IK2"
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/bound_moiety= "
831..837
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/bound_moiety= "
1809..1819
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/bound_moiety= '
1685..1698
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1597..1607
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590..596
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1524..1545
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803..812
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1076..1089
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                                                                                                                                                1180 CCCTTGGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGCGCGAGCCCCGAGCCCAGCGCTT 1235
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                                                                                                                                                                                                                                                      1360 TCGTGGGCGGCTGAACGTCGCCCGTTTAAGGGGGGCCCCGGGTCCACGTGCTTTCTGC 1419
                                                                                                                                                                                                                                                                                        Human, ATP-binding cassette 1, ABC1 gene regulation, atherosclerosis, cholesterol metabolism, hypercholesterolaemia; antisense therapy, ds.
                   940 AAGTOCAGGTTTGTGGGGGGAAAACAAAAGCAGCCCATTACCCAGAGGACTGTCCGCCTT
                                            1018 GCTITGACCGATAGTAACTCTCTGCGCTCGCTCGCTGCGCAAICTATAAAAGGAA 1070
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/*tag= a
/bound_moiety= "LMO2COM/NYOD"
97 .107
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196..211
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/bound_moiety= "DeltaEF1"
110..125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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228..237
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1642 CTTGAAGGGCAGATTCACATTTAGACTCTTCACAGTTTTGACCTGAGTTTTGGCCAGAATG 1583
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                                                                                                                                                                                                                                                                                                                                                                                                             241 ATGCCACCTCATTCTGGCCAAAACTCAGGTCAAACTGTGAAGAGTCTAAATGTGAATCTG 300
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cholesterol metabolism; hypercholesterolaemia; antisense therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                     Score 102.2; DB 24; Length 2910; Pred. No. 1.5e-17; 0; Mismatches 83; Indels 2;
                           '*tag= bd
'bound_moiety= "LM02COM/MYOD/E47"
                                                                                                                                                                                                      "USF/NMYC/ARNT"
                                                                                                                                                                                                                                                                                                                /*tag= bk
/bound_moiety= "GC/SP1/MZF1"
                                                                /*tag= be /bound_moiety= "RREB1" 2680..2698 /*tag= bf /bound_moiety= "MZF1/CMYB" 2728..2740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ABC1 transcription regulatory DNA #1
                                                                                                                                                                                                                                                                                     "XFD1/HEH"
                                                                                                                                                                                                                                              "NFE2AP1"
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/bound_moiety= "SP1/GC"
2743..2757
/*tag= bh
/bound_moiety= "MZF1"
2634..2648
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/bound_moiety= "
2774..2787
/*tag= "
/bound_moiety= "
2794..2806
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AAD37265/c
ID AAD37265 standard; DNA; 3231 BP.
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2758..2773
                                                                                                                                                                                                                                                                                                                                                      Query Match 6.7%;
Best Local Similarity 65.9%;
Matches 164; Conservative (
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bound_moiety= "HNF3beta/SRY/EVII"
426..2433
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bound_moiety= "IK2/NFkappaB/CREL"
259..2272
                                                                                                                                                                 *tag= ai
bound_moiety= "PPAR/NKX2.5/PPAR"
                                                                                                                                                                                                       *tag= aj
bound_moiety= "PPAR/NKX2.5/PPAR"
051..2059
                                                                                                                                                                                                                                                                                                                               *tag= am
bound_moiety= "SYR/HFH/HNF3beta"
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"pound_moiety= "STAT/PPAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag= aq
bound_moiety= "MZF1/SRY"
313..2318
                                                                                            bound_moiety= "HNF3beta"
978..1985
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bound_moiety= "NKX2.5"
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/bound_moiety= "AP2"
2610..2617
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bound_moiety= "PPAR"
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bound_moiety= "MZFl"
9442..2451
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bound_moiety= "PPAR"
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bound_moiety= "GATA"
104..2111
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bound_moiety= "SOX5"
114..2152
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bound_moiety= "STAT"
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491..2498
                                       /*tag- af
/bound_moiety= "AP1"
1942. 1956
              'bound_moiety= "SRY"
.840..1850
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/bound_moiety= "
2455..2466
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2361..2384
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                                                                                                                                                                              The invention relates a nucleic acid which is capable of regulating the transcription of human AIP-binding cassette 1 (ABC1) gene, which is a casual gene for pathologies linked to a dysfunctioning of cholesterol metabolism, including diseases such as atherosclerosis. Polynucleotides of the invention are used to screen candidate molecules or substances that are capable of medilating the transcription of the ABC1 gene. They are used in antisense therapy. Compositions comprising sequences of the invention are used to treat hypercholesterolaemia and atherosclerosis. The present sequence is human ABC1 transcription regulating DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - CTTGAAGGCCAGATTCACATTTAGACTCTTCACAGTTTGACCTGAGTTTTGGCCAGAATG 1583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1700 GAAGIGCACGIGGAGGC -- CACAAGGICICCTACCTIGACAAGATACCTTTGTAGCCAC 1643
                                                                                                                                                                                                                                                                                                                                                                                                                      1820 ATGICACCTIATTCTGGCCAAAACTCAGGTCAAACTGTGAAGAGTCTAAATATGAATCTG 1761
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                                                                                                     ucleic acid useful for modifying the ATP-binding cassette 1 screening for candidate modulatory compounds or substances
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTTCAAGGTGGCTACAAAGGTATCTTTGTCAAGGTAGGAGACCTTGTGGCCTCCAQGT
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                                     Denefle P;
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65.9%; Pred. No. 1.6e-17;
ive 0; Mismatches 83; Indels
                                     Lemoine C, Naudin L, Dene
ey A, Santamarina-Fojo S;
                                                                                                                                                                                                                                                                                                                 Sequence 3231 BP; 809 A; 773 C; 876 G; 773 T; 0 other;
                                                                                                                                                      Claim 1; Page 130-131; 152pp; English.
                                     Prades C, Lemoin
er N, Remaley A,
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                                                                                                       nucleic acid useful
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           (AVEI ) AVENTIS PHARMA SA
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 65.9
Matches 164; Conservative
                                     Rosier-Montus M, Pr
Brewer B, Duverger
                                                                           WFI; 2002-154404/20
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                                                                                                                (ABC1) and
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The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (ATP) binding cassette protein (ABC) I gene. ABCI resides in cell membranes and utilises ATP Aydrolysis to transport a wide variety of substrates across the plasma membrane. ABCI is a pivotal protein in the apolioporotein-mediated mobilisation of intracellular cholesterol stores. ABCI is defective in Tanglard ABCI is a pivotal cholesterol stores. ABCI is defective in Tanglard ABCI is a pivotal cholesterol stores. ABCI is defective in Tanglard ABCI genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes associated with hypercholesterolemia and atherosclerosis. The genes and proteins so to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.
                                                                                                                                                                                                                                                                                                                           nosine triphosphate (ATP) binding cassette (ABC) polynucleotide, tal for the development of agents for the treatment of heart disease other disorders associated with hypercholesterolemia and
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apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
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Pred. No. 3.2e-16;
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99US-0140264.
99US-0153872.
99US-0166573.
                                                                                                                               (CVTH-) CV THERAPEUTICS INC
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18-JUN-1999;
14-SEP-1999;
19-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (ATP) binding casette protein (ABC) I gene. ABCI resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABCI is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stories. ABCI is defective in Tangiar disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABCI gene is localised to chromosome 9q22-9q31. The ABCI genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulace the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and cher disorders associated with hypercholesterolemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTTCACGGCAGAITCATATTAGACTCTTCACAGTTTGACCTGAGTTTTGCCCAGAATA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AIGCCACCTCATICTGGCCAAAACTCAGGTCAAACTGIGAAGGTCTAAATGTGAATTTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCTTCAAGGTGGCTACAAAGGTATCTTTGTCAAGGTAGGAGACCTTGTGGCCTCCACGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCTGAAGGGAGATTCATAGAAGACTCAGGACAGACCCGTAGAAGAGGCCAAGCAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 IGGAAGIGCACGIGGAGGCCACAAGGICICCIACCIIGACAAAGAIACCIIIGIAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCACTTCCAGGGCCTGCTTGGCCTCTTCTACGGGTCTGTGCTGAGTCTTCTATGAATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                      Adenosine triphosphate (ATP) binding cassette protein (ABC) i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 97; DB 22; Length 1643;
Pred. No. 3.2e-16;
0; Mismatches 95; Indels
 chromosome 9922-9931; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1643 BP; 370 A; 413 C; 457 G; 403 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 138-139; 211pp; English.
                                                                                                                                                                                                                                                                                                                                 Garvin
                                                                                                                                                                                                 99US-0140264.
99US-0153872.
99US-0166573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.8%;
                                                                                                                                                               16-JUN-2000; 2000WO-US16591.
                                                                                                                                                                                                                                                                         CV THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                 GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154; Conservative
                                                                                                                                                                                                                                                                                                                                 Oram
                                                                                                                                                                                                                                                                                          (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-137811/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                Wade D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGTGGCAT
                                                                                         WO200078971-A2.
                                                                                                                                                                                                 18-JUN-1999;
14-SEP-1999;
19-NOV-1999;
                                                        Homo sapiens
                                                                                                                            28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                              Lawn RM,
                                                                                                                                                                                                                                                                         (CVTH-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301
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27714 AFGTCACCTTAFTCTGGCCAAAACTCAGGTCAAAACTGTGAAGAGTCTAAATATGAATCTG 27655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           selected
                                                                                                                                                                                                                 ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ATGCCACCTCATTCTGGCCAAAACTCAGGTCAAAACTGTGAAGAGTCTAAATGTGAATTCTG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating a lower than normal high density lipoprotein-choiesterol (HDL-C) level, a higher than normal tridyyceride level, or a cardiovascular disease, by administering a compound that modulates or RXR-mediated transcriptional activity
                                                                                                                                                                                                              High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27654 CCCTGAAGGACAGATTNCATAGAAGACTCAGGACAGACCCGTAGAAGAGGCCCAAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 GCACTICCAGGCCTGCTTGGCCTC---TTGTAGGGTGTGTGCTGAGTCTTGTATGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 CCCTTCAAGGTGGCTACAAAGGTATCTTTGTCAAGGTAGGAGACCTTGTGGCCTCCACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27594 CCCTGGAAGTGCACGTGGAGGCCACAGGTCTCCTACCTTGACAAGATACCTTTGTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCCCTTCAGGGCAGATTCATATTTAGACTCTTCACAGTTTGACCTGAGTTTTGGCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 183999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ASC1 expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition a lower than normal EDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clee SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pimstone SN,
     ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Fig 1; 317pp; English.
DNA; 183999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brooks-Wilson AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.0%;
ilarity 63.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0151977
                                                                                                                                                                                                                                                                                                                                                                                                                             01-SEP-2000; 2000WO-IB01492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0526193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0213958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (XENO-) XENON GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ABC1 genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        478 ATAAGGIGACAI 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-244356/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                       WO200115676-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUN-2000;
                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-1999;
                                                                                                        17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayden MR,
                                                    AAF92831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAR-
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RESULT 11

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RESULT 13 ABN80129

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The present invention describes an expressed sequence tag (EST), where the EST is an isolated, enriched, or purified nucleic acid sequence representing all or part of a gene, the expression of which, or its complementary sequence, in a cell identifies the cell as a developmentally competent or incompetent cell. Molecules which induce totipotence in one or more cells. Molecules which induce totipotence in one or more cells. Molecules which induce developmental incompetence in a cell line are useful for inducing totipotence. In a cell line are useful for preventing a full term pregnancy in an animal and inhibiting totipotence. The molecules are also useful for treating a disease in an animal by inducing development of one or more cells of the animal into a specific cell type. The present sequence represents a bovine EST which is given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    824 CTCCTTCCTCTCAAITTATGAAGAGAAGCAGTAAGATGTTCCTCTCGGGTCCTCTGAGGG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 AAGCAGGGAGCCCAAGCTTGCATCAGGCCCGTGCTGGGAGCCCCTGAAAAAAATCATTGC 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCTGGGGAGCTCAGGCTGGGAATCTCCAAGGCAGTAGGTCGCCTATCAAAATCAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 474;
                                                                                                                                                       EST; expressed sequence tag; totipotence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An expressed sequence tag (EST), the expression of which, o complementary sequence, in a cell identifies the cell as a developmentally competent or incompetent cell -
                                                                                                                   Bovine embryonic germ (EG) cell cDNA EST 990809a CONTIG 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 474 BP; 130 A; 109 C; 133 G; 102 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 51.4; DB 24;
Pred. No. 0.00067;
0; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                     childs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 16; Page 178; 584pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 ACATGATGATGAGGGCAGGAAGA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    944 CCAGGTTTGTGGGGGGAAAAAAAA 968
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eilertsen KJ, Pfister-Genskow M,
                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.4%;
                  ABN73478 standard; cDNA; 474
                                                                                                                                                                                                                                                                                                             07-JUN-2001; 2001WO-US18576.
                                                                                                                                                                                                                                                                                                                                                67-JUN-2000; 2000US-209874P.
06-JUN-2001; 2001US-0876143.
                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109; Conservative
                                                                                                                                                                        gene; ss.
                                                                                                                                                         taurus;
                                                                                                                                                                                                                                                                                                                                                                                                (INFI-) INFIGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-351289/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                          WO200194550-A2.
                                                                                                                                                                        development;
                                                                                    03-JUL-2002
                                                                                                                                                                                                                                                                           13-DEC-2001
                                                                                                                                                                                                          Bos caurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
                                                  ABN73478;
                                                                                                                                                         Bovine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
ABN73478/C
                   D.
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The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) of genes associated with development selected from 87 genes listed in the specification such as ACCPN, ADRN, or AFD1 and comprising one of 350 caseful for the diagnosis or their complements. The invention is sequences (ABN79984-ABN80333) or their complements. The invention is caseful for the diagnosis or their complements. The invention is development genes, in particular disease related to homeobox containing genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes associated with congenital heart disease, epilepsy, diseases, related to histone deacetylation, Currarino syndrome, diseases related with the checking the proper specific to each of the genes are useful for detecting the colligomers specific to each of the genes are useful for detecting the methylation state of all CpG dinuclectides within the 350 sequences or (II) and their complementary sequences, as primer oligomuclectides for the application of the 350 sequences, (II) and/or their complements and case single nucleotide polymorphisms (SNDS).

CC Single nucleotide polymorphisms (SNDS).

CC Note: The sequence data for this patent did not form part of the princed specification but is based on sequence information supplied to Derwent by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes associated with development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                      isuman, development; homeobox gene; HOX; diabetes; cancer; apoptosis;
heart disease; epilepsy; histone deacetylation; muscular dystrophy;
dwarfism; single nucleotide polymorphism; SNP; cytosine methylation;
antidiabetic; cytostatic; anticonvulsant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6116 BP; 1506 A; 214 C; 1527 G; 2869 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 146; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berlin K;
                                                                                                                    Human chemically modified disease
  BP.
DNA; 6116
                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043825.
                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-2001; 2001WO-EP07536.
                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIC-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-130908/17.
  ABN80129 standard;
                                                                                                                                                                                                                                                                                                                        WO200200927-A2.
                                                                                                                                                                                                                                                                sapiens.
                                                                               15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                              03-JAN-2002
                                         ABN80129;
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                                                                                                                                                                                                                                                                                 Syntheti
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The invention relates to human polynuclectides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leuksemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                     cell proliferation; cell differentiation; gene therapy;
                  Human, cytokine, cell proliferation; cell differentiation; gene the vaccine, peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
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                                                                                  Score 43.8; DB 2
Pred. No. 0.076;
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18-MAY-2000; 2000US-0577409.
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llarity 51.9%; Pred. No. 0.064;
Conservative 0; Mismatches 76; Indels 6;
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18-MAX-2000; 2000US-0577469
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Query Match

Best Loca Matches 685 317

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Search completed: February 3, 2003, 16:28:38 Job time : 933.553 secs Drosophil

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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (Dases I to 289)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Sllva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Brunstein,A., deolive,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            AL194922 Tetracdon
AL053013 Drosophil
AL05655 Drosophil
AL064271 Drosophil
BQ944204 AGENCOURT
AG081217 Pan Lrogl
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AL108536 Drosophil
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AL053013 Drosophil
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 ancar,
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CNS0080F
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AUTHORS
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AL056652 Drosophil
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AL066742 Drosophil AL108185 Drosophil BQ953024 AGENCOURI BG995916 MR4-H7119 BE012563 122176 MA AL554951 AL554951 AL657934 AL657934

AL430789 clone XBA

EST 28-APR-2000 mRNA sequence.

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AA527406
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This ending the feature of the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6at2=RC6-BT0252-271099-012-cl0&13=1999-10-27&14=1)
Seq primer: puc 18 forward High quality sequence start: 146 High quality sequence stop: 289.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 467)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Emall: cgabbs-r@mail.hin.gov
Tissue Procurement: Elias Campo, M.D., Michael R.,
Ph.D.
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Direct Submission Submitted (23-JuL-1999) Genoscope - Centre National de Sequencage : BP 19, 91006 EVX cedex - FRANCE (E-mail : seqrefagenoscope.cns.fr Determination of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out expand to the burphean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPE (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN15123 of DrosBAC library from Drosophila melanogaster (fruit
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image.html
Insert Length: 1657 Std Error: 0.06
Seg primer: -40ml3 fwd. EI from Amersham
Bigh quality sequence stop: 380.

1. .467
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosopiilidae; Drosophila.
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/db_xref="texon:7227"
/clone="BACN15123"
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/db_xref="taxon:9606"
/clone="IMAGE:936962"
/clone_lib="NCI_GGAP_C03"
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/tissue_type="colon"
/lab_host="DE108"
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Best Local Similarity 23.8%; Pred. No. 0.88;
Matches 86; Conservative 131; Mismatches 140;
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/db_xref="taxon:7227"
/clone="BACR11P16"
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon signoviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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1 (bases 1 to 298)

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1 Sest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Mincker, P., Brottler, P., Quetler, F., Saurin, W. and Weissenbach, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Boureau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Charaterization and repeat analysis of the compact genome of the freshwater pufferfish letraodon nigroviridis
                                                                                                                                                                                                                                                                                                                          1115 GGAAACTAACAAAGGAAAAAATTGCGGAAAGCAGCATTTAGAGGAAGCAAATTCCAC 1174
                                                                                                                                                                                                                            IGGTGCCCTTGGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGCGCAGCCCCGAGCCCAG 1234
                                                                                                                         Gaps
                                                                                                                                                                                                                                             CGCTTCCCGCCCGTCTTAGGCCGGCGGGCCGGGGGGGGAAGGGGACGCAGAGCGGGA
                                                                                                                                                                                                                                                                                                                                                            857 KRAAAMAAKWKTKMMTTGMARATMKKDTGGGMAATAAAGAAAAAWAAWDDDADTTKKK
                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                               1097 CCSSSSSCSGGGGGGGSGSGSCGNGGGGCSGGGGGGSSSGSSCCCGGSCSC 1148
                                                                                    Length 1201;
                                     157 others
                                                                                                                       Indels
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/db_xref="taxon:99883"
/clone="119N17"
                                                                                                                      132;
                                                                                     DB 17;
                                                                                    Score 60.8; DB
Pred. No. 0.032;
                                     Ļ
                                                                                                                      Mismatches
                                     235
/plasmid="pBelobACil"
/note="end : SP6"
276 c 278 g
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- Web: www.genoscope.cos.17)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruinfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gsoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genome survey sequence TEI3 end of BAC # BACRIP16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                          1180 CCCTTGGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGCGCAGCCCGAGCCCAGCGCTT 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1300 AGACACCTGCTGTACCCTCCACCCCACCCCACCCACCTCCCCCAACTCCCTAGATGTG 1359
                                                                                                                                                                                                                                                                           1240 CCCGCGCGTCTTAGGCCGGCGGGCCCGGGCGGGGAAGGGGACGCAGACCGCGACCCTA 1299
                                                                                                                                                                                82 CONKKSCCCVDVGCGCCVCSGSGSGSGSCCCSSCSSSSCCCCCCGGSGSSSGSCS 141
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Neoptera: Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 GSGSSCCSSCGSGSGSGGCCCCCSSVSGSGSGSGSGGGGCSCCSGSCGGCGCGCNATC
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When it is the state of the state of the state of a second and the state of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila meianogaster genome using these BACs. For further information please see http://www.fruitily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Manmoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y?: cn bw sp. the same strain used for the BDGP's pland and how to order individual BAC Clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://werpar.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                        GSS 03-JUN-1999
end of BAC #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
3P 191 91006 BVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                           Drosophila melanogaster genome survey sequence T7 end of BAC # \rm BACR14J21 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1118 AACTAACAAAGGAAAAAAATTGCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGG 1177
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                           Hexapoda; Insecta; Pterygota;
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 910)
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                               fly), genomic survey sequence. Al065629
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/note="end : T7"
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Matches
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AU222489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group)
Bukaryota, virdiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Pozles, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondal 2-1-2, Tsukiba, Ibaraki
305-8602, Japan
                                                                                                                                                          1237 CTTCCCGCGCCTCTTAGGCCGGCGGGCCGGGGGGAAGGGGACGCAGACCGCGGACC 1296
                                                                                                                                                                                                                                       1297 CTAAGACACCTGCTGTACCCTCCACCCCACCCCACCACCTCCCCCAACTCCCTAGAT 1356
                                                                                                                                                                                                                                                                                                                    GTGTCGTCGCCCCTTGAACGTCCCCCGTTTAAGGGGCGCGCCCCCGCCTCCACGTGCTTTC 1416
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                                     SASVSSACSSVAGSSMAAAGASCBGCAAANMCACGCSSSSSASRSRMMSSCSSCASSSCS 420
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                                                                             GIGCCCTTGGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGCCGCAGCCCCGAGCCG
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
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Sasaki,T. and Yamamoto,K.
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59.7%;
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Fax: 81-298-38-7468
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ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL

COMMENT

Neoteleostei;

Euteleostomi;

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CNS0091P 525 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                             Tetraodontidae; Tetraodon.

Tetraodontidae; Tetraodon.

Roest-Crollius (81)

Roest-Crollius (81)

Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Barntu, W. and Westsenbach, J.

Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostom
Actinopterygii, Meopterygii; Teleostei, Euteleostei, Neoteleost
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
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Bouneau,L., Billauic,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Charaterization and repeat analysis of the compact genome of freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Genoscope sequence ID : COAG132BE08SP1-end PUC-Ori"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission Submitted (12-APR-2000)
Submitted (12-APR-2000)
This sequence is a single read and was generated as iscale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 17; Length 681;
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/clone="132116"
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Tetraodon nigroviridis
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk · This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC and genet, in the DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Tetracocon nigroviridis genome survey sequence PCC-Ori end of clone
132116 of library G from Tetracocon nigroviridis, genomic survey
sequence.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefâgenoscope.cns.fr
                                                                                                                                               Drosophila melanggaster genome survey sequence T7 end of BAC BACN15808 of DrosBAC library from Drosophila melancgaster (fruit Ily), genomic survey sequence.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosopiilidae; Droscphila.
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/db_xref="taxon:7227"
/clone="BACN15208"
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38.6%; Pred. No. 2.9
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Determination of this BAC-end sequence was carried out as part of collaboration with the Backeley brosophila Genome Project (35GP). The BDGP is constructing a physical map of the Drosophila melanogaster agenome using these BACs. For further information please see http://www.fruitfly.org The BDGP brosophila melanogaster BAC library was prepared by Kazutoyo Googawa and Aaron Mammoser in Plater de Jong's laboratory in the Department of Canoer Genetics at the Roswell Park Canoer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECONI diselion of Prosophila DNA provided by the BDGP from the isogenic strain v2: on bw 8p, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalc.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (3-mail : seqrefégenoscope.cns.fr
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/db xref="taxon:7227"
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     genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                               Web: www.genoscope.crs.fr
Determination of this RAC-end sequence was carried out as part of collaboration with the Berkeley prosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila Aaron Mamoser 18AC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser 18AC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Suffalo, NY. The library is named RPCI-98 and was constructed by partial Scoral disestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                        Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91005 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fx
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1260
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                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neopiera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50.6; DB 17;
Pred. No. 3.6;
                                                                                                                                                                            Ephydroidea; Drosophillidae; Drosophila.
1 (bases 1 to 925)
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/clone_lib="RPCI-98"
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                                                                    Drosophila melanogaster.
Drosophila melanogaster.
                        GI:4934461
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nes 47; Conserv
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/tissue_type="large_cell carcinoma" / tissue_type="large_cell carcinoma" / the_host="DHIOB (phage-resistant)" / hotte="Organ: lung: Vector: proffs; site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-07721.F.
Pan troglodytes
Bukaryotes, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS 03-NOV-2001
AGENCOURT_8774721 NIH_MGC_18 Homo sapiens cDNA close IMAGE:6370362
5', mRNA sequence.
BQ944204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           into EcoRI/XhoI sites using the following 5' adaptor: GGCAGCAGG(6). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Supersoript IR T (Life Technologies). Note: this is a NIH MCC Library "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear GSS 03-NOV-200 genomic survey sequence.
                                                                                                                                                                                                                                          Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2542 row: m column: 19
High quality sequence start: 43
High quality sequence stop: 669.
Location/Qualifiers
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                                                                                                                                                                                                                                                            Mammalia; Butheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1004)
NIH-MCC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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52.0%; Fred. No. 9.6;
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Pan troglodytes DNA, clone: PIB-077321.F,
AG081217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/cb_xref="taxon:9606"
/clone="IMAGE:6370352"
/clone_lib="NIH_MGC_18"
                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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                                                                                             BQ944204.1 GI:22359682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazuchoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCORI diseation of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC sesource Center can be Location/Qualifiers

S Location/Qualifiers

S Location/Qualifiers
                                                                                                                                                                                   CNSOO6EZ 870 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of 3AC #
BACR13E15 of RPCI-98 library from Drosophila melanogaster (fruit
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Sukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Erachycera; Muscomorpha;
Ephydroidea; Drosophilidae; brosophila.
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/db_xref="taxon:7227"
/clone="BACR13E15"
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/note="end : TET3"
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Drosophila melanogaster genome survey secuence SP6 end of BAC
BACN03P19 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                       Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-Chou, Tsuruni: ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@sc.riken.go.jp, URL:http://ngp.gsc.riken.go.jp/, Tel.i81-45-503-9117, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PT3 This BAC end was generated during the R&D process and may have higher chance of
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Brachycera; Muscomorpha;
                Taylor, T.D., Yada, T.,
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1 (bases 1 to 1009)
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/db_xref="taxon:9598"
              Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Saxaki,Y. BAC end sequences of Library PTB
                                                                                                  Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Saxaki, Y. Direct Submission
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Pred. No.
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- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.ecgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns fr)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Length 1009;
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50; Mismatches
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Pred. No. 14
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ne : 2928.52 secs
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/organism="Drosophila
/db_xref="taxon:7227"
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/clone_lib="DrosBAC"
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85; Conserv
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Best Local 9
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Sequence 14, Applisequence 4, Applisequence 4, Applisequence 36, Applisequence 36, Applisequence 36, Appli
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18, Appl
11, Appli
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12, Appli
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13, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Appli
, Appli
3, Appl
                                                       2003, 12:56:40 ; Search time 71.9045 Seconds (without alignments) 6534.066 Million cell updates/sec
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Sequence 208,
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1 gaatteettgetggtggete.....ageegaatetataaaaggaa 1532
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Sequence 18
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US-08-483-533-4
US-08-483-533-4
US-09-283-471A-4
US-09-283-471A-36
PCT-US92-06532-1
US-09-149-476-24
US-09-149-476-24
US-08-149-476-24
US-08-149-476-24
US-08-149-476-24
US-08-149-476-24
US-08-149-604-1
US-08-3819-1
US-08-341-568-1
US-08-385-255-20
US-08-385-255-20
US-08-562-257-20
US-08-562-257-21
                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                   441362 segs, 153338381 residues
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                                                                                               US-09-596-141C-3_COPY_1_1532
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Maximum Match 100%
Listing first 45 summaries
                                       using sw model
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                                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length DB
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2320
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Sequence

Sequence 1, Appli Sequence 3, Appli Sequence 7, Appli Sequence 4, Appli Patent No. 5198345 Sequence 13, Appli Sequence 13, Appli D-20 Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 1, Appli	ATORY RESPONSES MP-140	DB 6; Length 2989; s 42; Indels 0; Gaps 0; rGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	VIRUS On # i 25
1934 4 US-08-776-844-1 1117 4 US-09-247-3733-3 4085 1 US-08-072-574-9 1907 4 US-08-072-574-9 1907 4 US-08-061-376-4 130 6 5198345-15 796 1 US-08-061-376-4 1132 6 S198345-15 794 1 US-08-0694-3 2378 4 US-08-0694-3 2378 4 US-08-0694-3 2378 4 US-08-368-134-10 2643 4 US-09-363-745-10 11529 4 US-09-103-840A-1 11529 4 US-09-103-840A-1 11529 4 US-09-361-745-4 1074 3 US-08-248-332-67 1074 3 US-08-248-332-67	RESULT 1 5378464 1/c ; Patent No. 5378464 ; APPLICANT: MCEVER, RODGER P. TITLE OF INVENTION: MODULATION OF INFLAMMATORY RE; BY ADMINISTRATION OF GMP-140 OR ANTIBODY TO GMP-140 ; CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/07/320,408 ; SEQ ID NO:1: LENGTH: 2989	2.8%; Score 42.8; 61.8%; Pred. No. C. C. tive 0; Mismatche TTGTTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	WLPOX
44 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	15.T 1 464-1/C ent No. 5378464 APPLICANT: MCEVER, RODE TITLE OF INVENTION: MOI NUMBER OF SEQUENCES: 32 CURRENT APPLICATION DAT APPLICATION DAT PILING DATE: 08-MAR-1 ID NO.1: 1 D NO.1: 144-1	Match Local Si es 68; 76 TATTG 1111 86 AATTT 111	US-00-232-463-14 Sequence 14, Application US/08232463 Sequence 14, Application US/08232463 Sequence 14, Application US/08232463 Sequence 14, Application US/08232463 SPELICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMBINANT FOWE, NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: ADDRESSE: Foley & Lardher STREET: 1800 Diagonal Road, Suite STRATE: VA COUNTRY: USA ZIP: 22312-0299 ZIP: 22312-0299 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: DARWING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PARENTE FORM: MEDIUM TYPE: Floppy disk COMPUTER: PARENT PRESIDE FORM: MEDIUM TYPE: Floppy disk COMPUTER: PARENT SYSTEM: PC-DOS/MS-DOS SOFTWARE: PARENTEN RELEASE FILO, VG.
000000000000000000000000000000000000000	RESULT 537844 ; Pated ; BY AF ; BY AF ; SEQ 1	Query Best I Match Oy 77 Db 299 Qy 83	S C C C C C C C C C C C C C C C C C C C

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1171 CCACTGGTGCCCTTGGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGGGGCGAGCCCGGAGC 1230
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WENTION: Method For Treating Tumorigenic Diseases
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South Wacker Drive
                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENI APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.5%; Score 38.8; DB 4; 49.2%; Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                    NAME: Zeller, James P.
REGISTRATION NUMBER: 28,491
REFENCE/DOCKET NUMBER: 26097/32742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/419,853
FILNG DATE: 11.APR-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/861,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09283471A Patent No. 6340673
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Tower, 233
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6300 Sears Tower,
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                                                                                                                                                                                                                                                                FILING DATE: 31-MAR-92
ATTORNEY/AGENT INFORMATION:
                                                                                                                    FILING DATE: 07-MAR-95
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 595 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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Best Local Similarity
Matches 131; Conserv
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CITY: Chicago
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    418 CTCCCTTCAGGGCAGATTCAIATTTAGACTCTTCACAGTTTGACCTGAGTTTTGGCCCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.7%; Score 40.6; DB 1; Length 7218; Best Local Similarity 4.2%; Pred. No. 0.34; Matches 13; Conservative 171; Mismatches 125; Indels 0
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South Wacker Drive
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Sequence 4, Application US/08483533

Patent No. 6172017

Patent No. 6172017

Patent No. 6172019

Patent No. 6172019

APPLICANT: Roizman, Bernard

APPLICANT: Chou, Joany

TILE OF INVENTION: Method for Treating Tumorigenic

TILE OF INVENTION: Diseases

NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                        30472/114 IMMU
                                                                                                                    APPLICATION NUMBER: EP 91 114 300.6
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APPLICATION NUMBER: US/08/232,463
FILING DATE:
                                                                              APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Marshall, O'Toole,
6300 Sears Tower, 233
                                                                                                                                                                         NAME: BENT, Stephen A. REGISTAATION NUMBER: 29,768
REGISTAATION NUMBER: 30,4
REFERENCE/JOCKET NUMBER: 30,4
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                        Independence (1997)

TELES: 899149

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                       FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                 (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS: ADDRESSE: Marshall,
                                                         PRICE APPLICATION DATA:
                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-232-463-14
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CITY: Chicago
                                                                                               FILING DATE:
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TELEPHONE: 312/474-6303
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3
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                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                               11-APR-95
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Best Local Similarity 49.29
Matches 131; Conservative
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                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        James P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                               FILING DATE: 11-APR-9
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
                                   ZIP: 60606-6402
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                      NAME: Zeller, Jame:
REGISTRATION NUMBER
                                                                                      COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
 Illinois
                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-283-471A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-483-533-36
                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1348 ICCCTAGATGTGTCGTGGGCGGCTGAACGTCGCCCGTTTAAGGGGCGGCCCCGGCTCCA 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.5%; Score 38.8; DB 4; Length 595; Best Local Similarity 49.2%; Pred. No. 0.33; Matches 131; Conservative 0; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: Method for Treating Tumorigenic NUMBER OF SEQUENCES: 43 CORRESPONDENCE ADDRESS: STREET MATCHT.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATUR SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                        27373/32742A
                                                           US/09/283,471A
04-APR-1999
N: 514
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                                                                                                                                      PRIOR APPLICATION DAIA:
APPLICATION NOBER: 07/861,233
FILING DATE: 31-MA-1992
PRIOR APPLICATION DATA:
APPLICATION NOBER: 08/419,853
FILING DAIE: 11-APP-1995
PRICR APPLICATION DATA:
APPLICATION NOBER: 08/419,533
FILING DAIE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 36, Application US/08483533
Patent No. 6172047
GENERAL INFORMATION:
APPLICANY: Roizman, Bernard
APPLICANY: Chou, Joany
                                                                                                                                                                                                                                                                                                                                      28,491
                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                          312/474-6300
312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 595 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                    CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                     NAME: Zeller, James P. REGISTRATION NUMBER: 2
                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                          FELEPHONE:
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US-08-483-533-36
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1171 CCACTGGTGCCCTTGGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGCGCAGCCCCGAGC 1230
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STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
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49.2%; Pred. No. 0.48;
tive 0; Mismatches 132;
                                                                                                                                    SOFIWARE: Patentin Release #1.0, Version #1.25
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United States of America
                                                                                                                                                                               APPLICATION NUMBER: US/08/483,533 PILING DATE: 07-MAR-95 CLASSIFICATION: 514
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                                                              :: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                          08/419,853
                                                                                                                                                                                                                                                                                                                                           07/861,233
                                                                                                                                                                                                                                                                                                                                                                                                                                    28,491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Roizman, Bernard
APPLICANT: Chou, Joany
TITLE OF INVENTION: Method I
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ATTORNEY/AGENT INFORMATION:
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1171 CCACTGGIGCCCTIGGCTGCCGGGAACGTGGACTAGAGAGTCIGCGGCGCAGCCCCGAGC 1230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
                    Suite 2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         best Local Similarity 49.2%; Pred. No. 0.48; Atches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
                                                                                                                                                                                                                                                                                                                               27373/8235
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EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
                  Two First National Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      788 GGCCCCCGAGCGGCCGACCGGGCT 813
                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 208, Application US/09149476
Patent No. 6420526
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/346-5750
                                                                                                                                                                                                                                                                                                            30,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                         CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
                                                                                                                                                                                                                                    19910910
                                                                                                                                                                                                                                                                                         NAME: Gruber, Lewis S. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                  312/984-9740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEIC ACID
EDNESS: single
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
     Bickhell
   Abban.
SIREET: 'Two
CITY: Chicago
-'me: Illinois
                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                      FILING DATE:
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                                                                                            60603
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TELEX: 2
                                                                                                                                                                                   SOFTWARE:
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                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query March 2.5%; Score 38.8; DB 4; Best Local Similarity 49.2%; Pred. No. 0.48; Marches 131; Conservative 0; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 27373/32742A
ELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
Illinois
United States of America
                                                                                                                                                              US/09/283,4718
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; Sequence 1, Application PC/"US9106532
; GENERAL INFORMATION:
APPLICANT: ROCZMAN, Bernard
                                                                                                           PC-DOS/MS-DOS
                                                                                                                                                                                                                                             AFFILAND DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/419,853
                                                                                                                                                                                                                                                                                                      FILING DATE: 11-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/483,533
FILING DATE: 07-UON-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                      IBM PC compatible
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INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                             04-APR-1999
1: 514
                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 1327 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                    Zeller, James P.
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                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER: (
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CORRESPONDENCE ADDRESS:
                                                    COMPUTER READABLE FORM:
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                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                               FILING DATE: 04
CLASSIFICATION:
                                   60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                          COMPUTER:
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Length 1335; Indels

EARLIER APPLICATION NUMBER: 60/040,625
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/046,336
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER APPLICATION NUMBER: 60/040,610
EARLIER PILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,507
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER APPLICATION NUMBER: 60/047,617 REFILING DATE: 1997-03-07
REPLICATION NUMBER: 60/040,625
RETLING DATE: 1997-03-07
REPLICATION NUMBER: 60/04C,334
REPLICATION NUMBER: 60/04C,336
REPLICATION NUMBER: 60/04C,336
REPLICATION NUMBER: 60/04C,336
REPLICATION DATE: 1997-03-07 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,632 FILING DATE: 1997-05-23 FILING DAIE: 1997-04-11 APPLICATION NUMBER: 60/043,669 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,312 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,313 UMBER: 60/047,618 1997-05-23 APPLICATION NUMBER: 60/047,492 FILING DAIE: 1997-05-23 APPLICATION NUMBER: 60/047,598 APPLICATION NUMBER: 60/043,568 FILING DATE: 1997-04-11 ING DATE: 1997-04-11 LICATION NUMBER: 60/043,671 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,674 APPLICATION NUMBER: 60/047,613 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,582 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,596 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,612 LICATION NUMBER: 60/047,601 ING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,580 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,314 60/043,569 LICATION NUMBER: 60/043,311 1997-05-23 JMBER: 60/047,592 1997-05-23 MBER: 60/047,581 1997-05-23 APPLICATION NUMBER: 60/047,584 FILING DATE: 1997-05-23 60/047,500 APPLICATION NUMBER: 60/047,587 FILING DATE: 1997-05-23 60/047,503 APPLICATION NUMBER: 60/038,621 1997-04-11 DATE: 1997-05-23 997-05-23 1997-04-17 1997-04-LICATION NUMBER: FILING DATE: 1997-09 APPLICATION NUMBER: FILING DATE: 1997-09 FILING DATE: 1997-05 APPLICATION NUMBER: FILING DATE: 1997-09 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: FILING DATE: ILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING TLING EARLIER , EARLIER , EARLIER , EARLIER BARLIER BARLIER EARLIER EARLIER EARLIER EARLIER SARLIER

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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11
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EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
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UMBER: 60/040,334
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FILING DATE: 1997-0
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
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CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,152
EARLIER APPLICATION NUMBER: 60/040,333
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...mer: 60/047,501
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APPLICATION NUMBER: 60/049,510
THE DATE: 1997-06-13
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EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FLING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,908
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APPLICATION UNBER: 60/048,964
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/057,650
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EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-32
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APPLICATION NUMBER: 60/056,876
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APPLICATION NUMBER: 60/056,909
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APPLICATION NUMBER: 60/056,862
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   FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,578
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APPLICATION NUMBER: 60/043,576
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APPLICATION NUMBER: 60/056,664
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APPLICATION NUMBER: 60/056,881
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US-09-149-476-24/c
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Best Local Similarity 55.99
***Ahes 56; Conservative
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EARLIER APPLICATION NOMBER: 00/048,974
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EARLIER APPLICATION NUMBER: 00/056,887
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 00/056,893
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EARLIE TR FILING DATE: 1997-05-23
TR PELING DATE: 1997-05-23
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TR APPLICATION NUMBER: 60/047,593
TR FILING DATE: 1997-05-23
TR PELING DATE: 1997-05-23
TR PELING DATE: 1997-05-23
TR PELING DATE: 1997-05-23 1997-08-22 JMBER: 60/047,595 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,590 UMBER: 60/056,892 1997-08-22 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,599 FILLING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,586 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,594 APPLICATION NUMBER: 60/047,588 60/047,585 APPLICATION NUMBER: 60/056,845 60/057,762 APPLICATION NUMBER: 66/043,315 1997-08-22 1997-05-23 1997-05-23 1997-05-23 APPLICATION NUMBER: FILING DATE: 1997-06 APPLICATION NUMBER: FILING DATE: 1997-01 APPLICATION NUMBER: FILING DATE: 1997-00 APPLICATION NUMBER: FILING DATE: FILING DATE: EARLIER I EARLIER A EARLIER I EARLIER PEARLIER PEAR EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER A EARLIER B EARLIER B EARLIER B EARLIER B EARLIER SARLIER SARLIER

0 DB 4; Length 2323; Indels 2.5%; Score 38.6; DF ilarity 65.9%; Pred. No. 0.7; Conservative 0; Mismatches EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER APPLICATION NUMBER: 60/056,654
EARLIER APPLICATION NUMBER: 60/056,654
EARLIER APPLICATION NUMBER: 60/056,654 EARLIER FILING DATE: 1997-06-13 EARLIER APPLICATION NUMBER: 60/061,060 EARLIER FILING DATE: 1997-10-02 EARLIER FILING DATE: 1997-09-05 EARLIER APPLICATION NUMBER: 60/049,610 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,909 60/057,650 EARLIER APPLICATION NUMBER: 60/057,669 APPLICATION NUMBER: 60/043,576 FILING DATE: 1997-04-11 60/056,875 60/056,862 60/056,887 60/056,908 60/048,964 ION NUMBER: 60/056,884 60/056,876 188,956,881 2222 AAITTATTAAATAAGAACAAGCAT 2198 836 AAITTATGAAGAGAAGCAGTAAGAT 860 997-08-22 90-90-266 1997-09-05 1997-08-22 1997-08-22 1997-08-22 1997-08-23 EARLIER APPLICATION NUMBER: 60, EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60, 997-08-2 EARLIER APPLICATION NUMBER: EARLIER FILING DATE: 1997-06 EARLIER APPLICATION NUMBER: EARLIER FILING DATE: 1997-06 EARLIER APPLICATION NUMBER: EARLIER FILING DATE: 1957-06 EARLIER APPLICATION NUMBER: EARLIER FILING DATE: 1997-06 EARLIER APPLICATION NUMBER: EARLIER FILING DATE: 1997-0 EARLIER APPLICATION NUMBER: Local Similarity nes 56; Conserv EARLIER FILING DATE: DATE: EARLIER FILING DATE: EARLIER FILING D Query Match Matches q ŏλ

Gaps RESULT 10 US-09-041-886-18

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GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharnoz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72 Patentin Release #1.0, Version #1.25 E: Campbell & Flores LLP 4370 La Jolla Village Drive, Suite 700 ZIP: 92122 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS Sequence 18, Application US/09041886 Patent No. 6235872 STREET: 43.0 ... STREET: 43.0 ... STREET: 43.0 ... STREE: California STATE: California ... STREE: California ... STREE: California ... STREET: California ... ST CORRESPONDENCE ADDRESS: ADDRESSEE:

SOFTWARE:

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Lexington
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US-08-829-839-1
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; LOCATION:
US-08-709-838-1
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US-08-829-839-1
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'atent No. 614000*.
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Moser, Bernhard
APPLICANT: Moser, Bernhard
"THIE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
"THIE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.5%; Score 38.6; DB 4; Length 4481; 52.1%; Pred. No. 0.95; Tive 0; Mismatches 79; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TKI96-01
TELECOMAUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
                                                                         ATTORNEY/AGENT INPORMATION:
NAME: Campbell, Cathry: A.
REGISTATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INPORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/709,838
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
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US-08-709-838-1
. Sequence 1, Application US/08709838
; Patent No. 5140064
                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                     TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 4481 base pairs
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Matches 86; Conservative
                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION: 530
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LOCATION: 163..4099
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                                                          CLASSIFICATION:
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US-09-041-886-18
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STATE:
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APPLICANT: Loctscher, Marcel APPLICANT: Loctscher, Marcel APPLICANT: Moser, Bernhard APPLICANT: Moser, Bernhard APPLICANT: Moser, Oin, Shixin TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3, TITLE OF INVENTION: ANTISODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR CORRESPONDENCES: 4

CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                     Length 1670;
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                                                                                                                                                                                                                                                                                                   43;
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Best Local Similarity 59.8%; Pred. No. 0.78;
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REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: Trig6-01A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NOMBER: US 08/709,838
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JMBER: US/C8/829,839
31-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6184358
GENERAL INFORMATION:
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(617) 861-9540
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1670 base pairs TYPE: nucleic acid STRANBEDNESS: double TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .670 base pairs
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SEQUENCE CHARACTERISTICS:
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EDNESS: double
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FILING DATE: 31-MAR:
CLASSIFICATION: 435
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OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
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OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
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LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ
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OTHER INFORMATION: Polymorphic fragment 5-127-261
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       OTHER INFORMATION: 5-133-375
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LOCATION: 88050..88096
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LOCATION: 88050..88096
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NAME/KEY: allele
LOCATION: 146328
OTHER INFORMATION:
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LOCATION: 150329
CTHER INFORMATION:
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LOCATION: 108308
OTHER INFORMATION:
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LOCALION: 108471
OTHER INFORMATION:
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LOCATION: 134374
OIHER INFORMATION:
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LOCATION: 146345
OTHER INFORMATION:
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                                                                                NAME/KEY: allele
LOCATION: 108149
OTHER INFORMATION:
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             VILLE:
VAME/KEY: allele
"""TON: 108106
                                             LOCATION: 108106
OTHER INFORMATION:
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NAME/KEY: allele
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LOCATION: 134134
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NAME/KEY: allele
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                                                                                                                                                                                                                      GENERAJ INFORMATION:
APPLICANT: BOGGUELECEL, LYGIE
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBF-7)
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: GENSEI.031A
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                                                                       714 ICCTGTGTTTTTATCACAGGGAGGCTGATCAATATGAAATTAAAAGGGGGGCTGGTCC 773
                                  Gaps
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         Length 1670;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   deletion
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                                 43; Indels
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      Score 38.2; DB 4;
Pred. No. 0.78;
0; Mismatches 43;
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                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1995-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1988-12-10
PRIOR FILING DATE: 1988-12-10
NUMBER OF SEQ ID NOS: 140
SEQ ID NO 1
                                                                                                                                                                                             Sequence 1, Application US/09345882
Patent No. 6395373
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59.8%;
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Query Match
Best Local Similarity 59.8%
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LOCATION: 93714
OTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
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OTHER INFORMATION:
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OTESE INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: allele
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LOCATION: 106940
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90842
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LOCATION: 97122
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US-09-345-882-1/c
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NAME/KEY:
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Db 109593 TARACTITITIACTATATICATATARAGCCCCATTITITIATTITICCCCTTCCTGTTCGT 109534
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VENTION: DNA Sequences Encoding Kutant Antiviral
VENTION: Regulatory Proteins
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                                                                                                                                                                                         Db 109473 TITTITITITITIGAGACAGACTCICACTCGATCCCCCAAG 109433
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COMPUTER READABLE FORM:
MEDIUK TYPE: Diskette, 3.50 inch, 720 Kb storage
                                                                                                                                                     806 TITITITITITITICIGCCTCCTTCCTCTCAATTIATGAAG 846
                                                                                                                                                                                                                                                                                                                                                                                                                                             The Pennsylvania State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.5%; Score 37.6; DB 54.3%; Pred. No. 0.87; ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Microsoft Word for Windows 6.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/018,977C
FILING DATE: 18-FEB-1993
CLASSIFICATION: 435
RUCR APPLICATION DAIR: APPLICATION NUMBER: 07/726,671
                                                                                                                                                                                                                                               RESULT 14
US-08-018-977C-4/c
Sequence 4, Application US/08018977C
Patent No. 56866C1
GENERAL INFORMATION:
APPLICANT: Webber, Peter C.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSE: The Pennsy.....STREET: 113 Technology Center
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REFERENCE/DOCKET NUMBER: 91.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (814) 665-6277
TELEFAX: (814) 865-3591
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

US-08-018-977C-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University Park
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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SOFTWARE: Microsc
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Best Local Similarity
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                                                                                               LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
                                                                                                                                                                                             INFORMATION: polymorphic fragment 99-1442-224 SEQ ID73
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OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
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                                                                                                                                                                                                                                                                     SEQ ID33
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                                         OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
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OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ
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LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276
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OTHER INFORMATION: polymorphic fragment 5-131-395
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OTHER INFORMATION: polymorphic fragment 5-129-144
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OTHER INFORMATION: polymorphic fragment 5-136-257
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LOCATION: 106918..106965
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LOCATION: 97099..37145
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93590..93736
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OTHER INFORMATION:
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LOCATION: 106918.
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NAME/KEY: allele
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LOCATION: 103783.
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     NAME/KEY: A
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Gaps

2.5%; Score 37.8; DB 4; Length 162450; 52.2%; Pred. No. 8.4; Indels 0; Mismatches 77; Indels 0;

Query Match
Best Local Similarity 52.23
Matches 84; Conservative

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SESSIENT 18

SUSTEME 1. APPLICATION

SEQUENCE 1. APPLICATION

PRAPELICANI TREPRANCION

APPLICANI TREPRANCION

TITLE DE INVENTION: Muclease having altered specificity

NUMBER OF SECURATES.

COMPANIENCE ADDRESS:

COMPANIEN
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Db 699 AITGAAAGAAGCAGTGATTGGTTAACACAGGTCC 665

841 ATGAAGAGAAGCAGTAAGATGTTCCTCTCGGGTCC 875

Db Qy Search completed: February 3, 2003, 16:23:20 Job time : 304.905 secs

DNA seq

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Searched:

Database

Result No.

128450680

Sequence:

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HSV-1 (P) ICPA:5
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Nucleotide sequenc
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Human ABCAi homolo
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ABC1 polymorphism
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Human ABC1 DNA se
Human ABC1 gene e
Human cDNA clone
                                                                                                                                                                                                                                                                                                        Genomic sequence
                                                                                                                                                                                                                                                                                   Sequence encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of the 5' flanking region of the human ABCl gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, adenosine triphosphate binding cassette protein 1, A301; apolipoprotein-mediated mobilisation, cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cholesterol transport; ss
                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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AAT95102
AAQ97701
AAS76999
ABK83571
AAA64196
AAN70930
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AAS42003
AAK87230
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AAF24707
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 (CVTH-) CV THERAPEUTICS INC
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atherosclerosis;
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14-SEP-1999;
19-NOV-1999;
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Compugen Ltd.
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           GenCore version Copyright (c) 1993 - 2003
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Perfect score:
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RRV genome nucleot

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AAF24703 standard; DNA; 1643 BP

(first entry)

20-APR-2001

AAF24703;

Nucleotide sequence

of the 5' flanking region of the human ABC1 gene.

Human: adenosine triphosphate binding cassette protein 1; A3C1; applipoprotein-mediated mobilisation; cholesterol; Targier disease; chromosome 9422-941; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.

WO200078971-A2.

16-JUN-2000; 18-JUN-1999; 14-SEP-1999; 19-NOV-1999;

28-DEC-2000

Homo sapiens.

```
The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABC1 resides in cell membranes and utilises ATP indroysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tanger disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and ciner disorders associated with hypercholesterolemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for
                  Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      are also useful as diagnostic indicators of cardiovascular disease other discreers associated with hypercholesterolemia.
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                                                                                                                                                                  Claim 1; Page 143-144; 215pp; English.
                                                                                                               atheroscierosis
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1080 GAGCICICICCCCCCAALCCCICCCCCCCAGGAAACIAACAAAAAAAAT 1139
                                                                                                                                         1200 SGACTAGAGAGTCTGCGGCGCAGCCCCGAGCCCAGCGCTTTCCCGCGCGTCTTAGGCCGGC 1259
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                                                                                                                          61 TGCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGT 120
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                                 Gaps
                                                             1 GAGCTCTCTCTCCCCCATCCCTCCCTCCGGCTGAGGAAACTAACAAAGGAAAAAAT 60
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                               0;
 DB 22; Length 1643;
                                 Indels
100.0%; Score 564; DB 22; 100.0%; Pred. No. 3.9e-140;
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nes 564; Conservative
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Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and

Garvin M;

Oram JF,

Wade D,

Lawn RM,

WPI; 2001-137811/14.

CV THERAPEUTICS UNIV WASHINGTON.

(CVTH-) CV

(MINO)

99US-0153872. 99US-0166573.

Disclosure; Page 138-139; 211pp; English.

atherosclerosis

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The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (ATP) binding cassette protein (ABC) I gene. ABCI resides in cell membranes and utilises ATP Mydrolysis to transport a wide variety of substrates across the plasma membrane. ABCI is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholestrol stores. ABCI is defective in Tanglac disease, a genetic chorder obstacted by abnormal HDL-cholesterol metabolism. The ABCI gene is localised to chromosome 9422-9431. The ABCI genes and proteins are iseful for developing pharmaceutical agents for the treatment of neart disease and other disorders associated with hypercholesterolemia and atheroscierosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorded with hypercholesterolemia.
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1619

1500 CTGCGCTCGGTGCAGCCGAATCTAIAAAAGGAACTAGTCCCGGCAAAAACCCCCGTAATIG 1559

11560 CGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGCCGAGCCGACCTTCTCCCCGGGCT

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RESULT 2 AAF24703

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Length 1197;

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transfer vector encodes and expresses a reporter molecule. The method further involves introducing into the cell a gene transfer vector comprising a nucleic acid segment encoding a transactivator protein the transactivator protein the transactivator protein, or an agonist of the transactivator protein, with the transactivator protein, and agonist of the transactivator protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 AACGGGGGGGGGAGAGAGAGAGACACCAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGGGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAACAGAGGCCGGG 989
                                                                                                                                                                                                                                                                                                                                                                                     73 GATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGTGGACTAGAGAGT 132
                                                                                                                                                                                                                                                                                                    atherosclerosis. The present sequence represents the hABC1 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1;
                                                                                                                                                                                                                                                                                                                         133 CTECGGCGCAGCCCGAGCCCAGCGCTTCCCGCGCGTCTTAGGCCGGCGGGCCCGGGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTGGGCCGGCACCCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGCCAGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 GGGAAGGGGACGCAGACCCGGGGGACCCTAAGACACCTGCTGTACCCTCCACCCCCACCCCCA
topical application to the cell or microinjection.
                                                                                                                                                                              Sequence 1197 BP; 284 A: 314 C; 328 G; 271 I; 0 other;
                                                                                                                                                                                                                   97.9%; Score 552; DB 24; L
100.0%; Pred. No. 5.6e-137;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                introducing into the host cell a gene transfer vector comprising the promoter operably linked to a foreign DNA encoding a desired polypeptide or SNA, where the foreign DNA is call by adenovirus infection, liposome-mediated introduced into the host cell by adenovirus infection, liposome-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human large ATP-binding cassette transporter i(hABC1) promoter sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated human large ATP-binding cassette transporter I promoter capable of directing transcription of heterologous coding sequence positioned downstream to it, useful for expressing foreign DNA in host
                                                                                                                                                                              The invention relates to an isolated human large ATP-binding cassette transporter 1 (ABC1) promoter capable of directing transcription of heterologous coding sequence positioned downstream to it. The hABC1 promoter is useful for expressing foreign DNA in a host cell, by
                                                                                                                                                                                                                                          420
                                                                                                                                                                                                                                                                                                                                                                                                        481 CGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCTTCTCTCCCGGGCT 540
                                                                                                                                                                                                                                                                                                                         421 CTGCGCTCGGTGCAGCCGAATCTATAAASGAACTAGTCCCGGCAAAAACCCCGTAATTG 480
                                                                              181 GGGCCGGGGGGGGAAGGGGACGCAGACCCGGACCCTAAGACACCTGCTGTATACCCTCC
                                                                                                                                                           361 ACAGAGGCCGGGAACGGGGCGGGGAGGAGGAGCACAGGCTTTGACCGATAGTAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; large ATP-binding cassette transporter 1; ABC1; promoter; antiarteriosclerotic; gene transfer; transactivator; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1620 GCGCCAGGGCAGGGGGGGGGGGGGGTC 1643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541 GCGGCAGGCAGGCGGGAGCTC 564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL-58400 standard;
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RESULT 3 ABL58400

GGGCTGCGGCAGGGCAGGCGGGGAGCTC 564

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28491
                                                                                                                                          Ireating a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardicvascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332
                                                                                                                                                                                                                 The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density inpoprotein-cholesterol (HDL-O) level, a higher than normal trigiveride level, or a cardiovascular disease, involving administering a compound that modulates LNR- or RNR-mediated transcriptional activity or ABCl expression or activity. The LNR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition lower than normal HDL cholesterol level, a higher than normal trigiyceride level, and a cardiovascular disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGACTAGAGAGTCTGCGGCGCAGCCCCGAGCCCAGCGCTTCCCGCGCGCTCTTAGGCCGGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                           IGCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACCTCTGCGCTCGGTGCTGAATCTATAAAGGAACTAGTCCCGGCAAAAACCCCGT
                                                                                                                                                                                                                                                                                                                                     Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;
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                                                                                                                                                                                                                                                                                                                                                         97.2%; Score 548; DB 22;
98.9%; Pred. No. 2.8e-135;
ive 0; Mismatches 1;
                                                                                                     Pimstone SN,
                                                                                                                                                                                                 Fig 1; 317pp; English.
                                                                                                     Brooks-Wilson AR,
                                                                      (UYBR-) UNIV BRITISH COLUMBIA.
                                     2000US-0526193.
2000US-0213958.
       2000WO-IB01492
                            99US-0151977
                                                                                (XENO-) XENON GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 98.9
Matches 563; Conservative
                                     2000; 2000US-
                                                                                                                         WPI; 2001-244356/25.
                                               23-JUN-2000;
       01-SEP-2000;
                            01-SEP-1999;
                                                                                                     Hayden MR,
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                 Claim 8;
                                        5-MAR
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The invention relates a nucleic acid which is capable of requiating the transcription of human ATP-binding cassette 1 (ABC1) gene, which is a casual gene for pathologies linked to a dysfunctioning of cholosterol metabolism, including diseases such as atherosclerosis. Polynucieotides of the invention are used to screen candidate molecules or substances that are capable of modulating the transcription of the ABC1 gene. They are used in antisense therapy. Compositions comprising sequences of the invention are used to treat hypercholosterolaemia and atherosclerosis. The present sequence is human ABC1 transcription regulating DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2416 GAGCTCTCTCTCCCCCAFTCCCTCCGGCTGAGGAAACTAACAAAAAAAAA 2475
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substances
                                                                                                                                                                                                                                                                                                                                           Human; ATP-binding cassette 1; ABC1 gene regulation; atherosclerosis; cholesterol metabolism; hypercholesterolaemia; antisense therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TGCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Denefle P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid useful for modifying the ATP-binding (ABC1) and screening for candidate modulatory compounds or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                 Human ABC1 transcription regulatory DNA #1.
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28952 GGCTGCGCCAGGCCAGGCGGGGAGCTC 28880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 130-131; 152pp; English
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98.98;
                                                                                                                                                  AAD37265 standard; DNA; 3231
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                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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/*tag= t
1189...1209
1189...1209
                                                                                                                                                                                                                              "DeltaEF1/LYF1/IK2"
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//bound_moiety= "PPAR/NKX2.5/PPAR"
2019..2024
/*tag= aj
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'bound_moiety= "USF/NMYC/MYCMAX"
                                                                                                      "HFH2/SRY/EVIl"
                                                                                                                                                                                                                                                                                                     'Dound moiety= "ZID/deltaEF1
1597..1607
'*tag= y
                                                                                                                     /*tag= p
/bound_moiety= "CREBP1/VBP"
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'pound_moiety= "DeltaEF1"
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                    /*tag= l
/bound_moiety= "NFY/CAAT"
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    /bound_moiety= "LKX2.5"
508..620
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/*tag= z
/bound_moiety= "PPAR"
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/bound_moiety= "MZF1"
771..785
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723..730
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1498..1514
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/bound_moiety= "
1978..1985
                                                                                       /bound_mciety= ".803..812
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/bound_moiety= "
1076..1089
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/bound_moiety= '
1840..1850
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1685..1698
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942..1956
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2008..2016
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/bound_moiety=
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1483..1491
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bound_moiety=
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**tag= ac
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2716 CGICGCCGTTTAAGGGGGGGGGCCCGGGTCCAGCGTGCTTTCTGCTGAGTGACTGAACTA 2775
                                                                                                                                                                                                                                                                                              Human, ATP-binding cassette 1, ABC1 gene regulation, atherosclerosis, cholesterol metabolism; hypercholesterolaemia, antisense therapy; ds.
                                                                                                              CGTCGCCCGTTTAAGGGGGGGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTA
                                                                                                       416 AACCICTGCGCTCGGTGCAGCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAAACCCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'bound_moiety= "LMO2COM/MYOD/DeltaEF1"
849..556
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/bound_moiety= "LMO2COM/MYOD"
97..107
                                                                                                                                                                                                                                                                                Human ABC1 transcription regulatory DNA #3.
                                                                                                                                                                                                                                                                                                                                                                                                             /bound_moiety= "S8/NKX2.5"
196..211
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590..596
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                                                                                                                                                                                2956 GGGCTGCGGCAGGGCAGGGGGGGGGGGCC 2984
                                                                                                                                                                       536 GGGCTGCGGCAGGCCGGGGGGGGCTC 554
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412..420
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228..237
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12..23
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528..539
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/*tag= au
/bound_moiety= "HNF3Deta/SRY/EVI1"
2426..2433
                                                                                                                            "IK2/NFkappaB/CREL"
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/bound_moiety= "PPAR/NKX2.5/PPAR"
2051..2059
                                                                           bound_molety= "SYR/HFH/HNF3peta"
221..2228
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                                                                                                                                                     "LMO2COM/GATA'
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2728..2740
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2680..2698
/*tag= b£
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bound_moiety= "MZFl"
361..2384
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bound_moiety= "PPAR"
:321..2326
                                                   /bousd_moiety= "soxs"
2114..2152
                                                                                                    bound_moiety= "MZF1"
                                                                                                                                                                                                                                "PPAR"
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/bound_molety= "MZF1"
2442..2451
                          /bound_moiety~ "GATA"
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/bound_moiety= "1
2634..2648
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/bound_moiety= ".
2657..2672
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/bound_molety= "
2289..2306
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/bound_molety= '
2491..2498
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2743..2757
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259..2272
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335..2342
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                                                                                                                                                                                                                                                                                                  2476 TGCGGAAAGCAGGATTTAGAAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCGGGAACGT 2535
                                                                                                                                                                                                                                                                                     GGGCCCGGGGGGAAAGGGGACGAGACCGGACCCTAAGACACCTGTGCTGTACCCTCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                     416 AACCICIGCGCICGGIGCAGCCGAAICIATAAAAGGAACIAGICCCGGCAAAAACCCCGT 475
                                                                                                                                                                                                                                            GGACTAGAGAGTCTGCGGCGCAGCCCCGAGCCCAGCGCTTCCCGCGCGCTCTTAGGCCGGC 180
                                                                                                                                                                                                61 IGCGGAAAGCAGGATTTAGAGGAAGCAAAITCCACTGGTGCCCTTGGCTGCCGGGAACGT 120
                                                                                                                                 Gaps
                                                                                                                                                    1 GAGCICICICCCCCAAICCCICCCICCGCTGAGGAAACTAACAAAGGAAAAAAAA 50
                                                                                                                                                                                                                                                       Score 473.4; DB 24; Length 2910; Pred. No. 5.6e-116; 0; Mismatches 1; Indels 5;
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                                                                            /*tag= bk
/bound_moiety= "GC/SP1/MZF1"
                                                      "XFDI/HFH"
         /*tag= bi
/bound_moiety= "NFE2AP1"
2774..2787
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2794..2806
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ilarity 98.8%;
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2758..2773
                                           /*tag= bj
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                                                                                                                     Similarity
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                                                                                                            Query Match
Best Local 9
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The present sequence is one of a large number of 5' ESTS derived from manas encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS water prepared from total human RNAs or polyat RNAS derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences of the second to the full suited for isolating cDNA sequences because they are obtained, the full 5' UTR is rarely included. S' ESTS are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in clasgostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human: ATP binding cassette transporter 1, ABC1; coronary heart disease; dermatological; atherosclerosis; cardiovascular; inflammatory disease; psoriasis; lipid disorder; antibacterial; septic shock; gene therapy; immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.2%; Score 119.4; DB 21; Length 227; 99.2%; Pred. No. 3.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ATP binding cassette transporter 1 (ABC1) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 227 BF; 44 A; 65 C; 73 G; 45 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Human ABC1 protein"
                                             Giordano J;
                                                                                                                                                                                    Claim 1; SEQ ID 1369C; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                               Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                               expression and secretion vectors
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                                               Dumas Milne Edwards J,
                                                                                WPI; 2000-500381/45.
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Best Local Similarity
              (GEST ) GENSET
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The invention relates to four common polymorphisms in the gene encoding ATP-binding cassette transporter-1 (ABG1). ABG1 is associated with ABG1 decreased ApgA-1 mediated efflux of cholesterol. The polymorphisms in ABG1 directly affects cellular lipid homeostasis, which is a key factor in the atherogenetic processes. The ABG1 polymorphisms are useful for diagnosing and treating lipid disorders, cardiovascular diseases (coronary heart disease, atherosclerosis) and inflammatory diseases (psoriasis, lupus erythematosus). The identification of ABG1 as a transporter for interleukin-lbeta (Li-lotta) identifies this gene as a candidate for treatment of inflammatory diseases including theumatoid arthritis and septic shock. The present sequence is human ABG1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467 AAACCCCGTAATTGCGAAGCGAGGAGTGGGGGCCGGGACCCGCAGAGCCGAAGCCGACCC 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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/note= "alternative open reading frame of AAI70314"
                                                                                                                                                               New adenosine triphosphare binding cassette transporter-1 gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiinflammatory; antilipaemic; antipsoriatic; dermatological; rangier disease; coronary heart disease; diagnosis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP binding cassette transporter 1; ABC1; human; lipid disorder; cholesterol; cardiovascular disease; inflammatory disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 7260;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7250 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 4.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     527 TTCTCTCCCGGGCTGCGGCAGGGCAGGCGGGGGGCTC 564
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100.0%; Piv
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                                                                                                                                                                                                                                Example 1; Fig 1; 48pp; English.
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20-MAR-2000; 2000EP-0105820
                              20-MAR-2000; 2000EP-0105820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                          Bodzioch
                                                                                                                        2001-640388/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 98; Conserv
                                                             (FARB ) BAYER AG.
                                                                                                                                      P-2SDB; AAE13022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sabiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JAN-2002
                                                                                          Schmitz G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI70315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
AAI70315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δğ
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variation

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21-AUG-2002 (first entry)
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                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH0743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ÓΫ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ö
                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of CDNA encoding the human adenosine triphosphate (ATP) binding cassette transporter 1 (ABC1) protein (see AAM50227). The sequence includes an extended open reading frame (ORF) to that provided by the sequence in AAI70314, using an alternative ATC codon as initiation codon and thereby adding an alternative ATC codon as initiation codon and thereby adding an alternative ATC codon as initiation of the encoded ABC1 protein (see AAM50228). The invention provides 4 common polymorphisms in the ABC1 gene. These were identified by sequencing the ABC1 gene in the AAI70314, G is changed to A at position 596, T is changed to C at position 136, A is changed to G at position 589 or G is changed to C at position 136, A is changed to G at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed to C at position 2589 or G is changed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         457 AAACCCCGTAATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAACCCCGTAATTGCCAGCGAGCGAGTGAGTGGGGCCGGGGCCGGAGCCGAGCCGACCC
                                                                                                                                                                                                                                                                                                            New adenosine triphosphate binding cassette transporter gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 7260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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4.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCTCTCCCGGGCTGCGGCAGGGCAGGGGGGGGAGCTC 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCTCTCCCGGGCTGCGGCAGGGCGGGGGGGGGGGCTC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No.
Matches 99; Conservative 0; Mismatci
                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 26-28; 41pp; English.
   /*tag= e
replace(3836,C)
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD37268 standard; DNA; 221
                                                                                                                             2000EP-0106401.
                                                                                                                                                              24-MAR-2000; 2000EP-0106401
                                /*tag=
                                                                                                                                                                                                                               G, Bodzioch
                                                                                                                                                                                                                                                              WPI; 2001-640389/74.
                                                                                                                                                                                              (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                               P-PSDB; AAM50228
                                                                                                                               24-MAR-2000;
                                                               EP1136554-A1
                                                                                                26-SEP-2001.
                 variation
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                                                                                                                                                                                                                                 Schmitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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Human, primer, detection, diagnosis, antisense therapy, gene therapy, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates a nucleic acid which is capable of regulating the transcription of human ATP-binding casette 1 (ABC1) gene, which is a casual gene for pathologies linked to a dysfunctioning of cholesterol metabolism, including diseases such as atheroscierosis. Polynucleotides of the invention are used to screen candidate molecules or substances that are capable of modulating the transcription of the ABC1 gene. They are used in antisense therapy. Compositions comprising sequences of the invention are used to treat hypercholesterolaemia and atheroscierosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, ATP-binding cassette 1; ABC1 gene regulation; atherosclerosis; cholesterol metabolism; hypercholesterolaemia; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             substances
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid useful for modifying the AFP-binding (ABC1) and screening for candidate modulatory compounds or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s C, Lemoine C, Naudin L, Den
Remaley A, Santamarina-Fojo S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 221 BP; 44 A; 62 C; 73 G; 42 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.le-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is human ABC1 gene exon 1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.1%; Score 91; DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA clone (5'-primer) SEQ ID NO:4267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.1
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      534 CCGGGCTGCGGCAGGGCAGGGCGGGAGCTC 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CCGGGCTGCGGCAGGCGGGGGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 132: 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.10.
100.08; Pir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prades C,
                                                                                                                                                                                                                                                                                                                                                   02-MAY-2001; 2001WO-3P05488.
                                                                                                                                                                                                                                                                                                                                                                                                              02-MAY-2000; 2000US-201280P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
Human ABC1 gene exon 1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brewer B, Duverger N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AVET ) AVENTIS PHARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-154404/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
tes 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosier-Montus M,
                                                                                                                                                                                                                                 WO200183746-A2
                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1074617-A2
                                                                                                                  1A; ds.
                                                                                                                                                                                                                                                                                            08-NOV-2001
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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                474 GTAATTGCGAGGGAGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTC 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GTAGTTGCGAGGGGAGAGTGAGTGGGGCGGGGACCCGCAGAGCCGAGCCGACCTTCTCTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 89.4; DB 22; Length 736; Pred. No. 4.3e-14;
                                                                                                 Saito K, Ya
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 736 BP; 163 A; 199 C; 199 G; 170 T; 5 other;
                                                                                                                                                                                      Claim 1; SEQ ID 4267; 2537pp + CD ROM; English.
                                                                                                           Nagai K,
                                                                                                Hayashi X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    534 CCGGGCTGCGGCAGGCAGGCGCGGGAGCTC 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CCGGGCTGCGGCAGGCCGGGGGGGCTC 91
                                                                                                sogai I, Nishikawa I, Hay
Sugiyama I, Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA sequence SEQ ID NO:18808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH18606 standard; cDNA; 1556 BP
                                 27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JON-2000; 2000JP-0241699.
                                                                                                                                                                                                                                                                                                                                                                                                                                15.9%;
        2000EP-0116126.
                          99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                             (HELI-) HELIX RES INST
                                                                                                                         WPI; 20C1-318749/34
                                                                                                Isogai I,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                      full-length cDNAs
        28-JUL-2000;
                          29-JUL-1999;
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06
                                                                                             Ota I, Is
Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE18606;
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db
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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; SEQ ID 18808; 2537pp + CD ROM; English.
                                                                                                                                         28-JUL-2000; 2000EP-0116126.
                                                                                                                                                                                                                   27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0193767.
                                                                                                                                                                                                                                                                                                                                           (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                         Isogai I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        full-length cDNAs
Homo sapiens
                                                                                                                                                                                          29-JUL-1999;
                                                                                                                                                                                                                                                                                        09-JUN-2000;
                                             EP1074617-A2
                                                                                           07-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                Ishii S,
The present invention describes primer sets for synthesising 5602

full-length cDNAs defined in the specification. Where a primer set

comprises: (a) an oligo-dT primer and an oligonuclectide complementary

to the complementary strand of a polynuclectide which comprises one of

complementary strand of a polynuclectides; or (b) a combination

of an oligonuclectide comprising a sequence complementary to the

complementary strand of a polynuclectide which comprises a 5'-end

sequence and an oligonuclectide compriser a 5'-end sequence complementary to a

complementary strand of a polynuclectide which comprises a 5'-end

sequence and an oligonuclectide compriser as sequence, where the

coligonuclectide which comprises a 3'-end sequence, where the

coligonuclectide which comprises as 1'-end sequence, where the

coligonuclectide comprises at least 15 nuclectides and the combination of

the 5'-end sequence/3'-end sequence is selected from those defined in

the specification. The primer sets can be used in matisense therapy and

conditionally full-length cDNAs. The primers are also useful for the

color particularly full-length cDNAs. The primers are also useful for the

color and/or dagmosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers allow obtaining of the full-length

colors as a sequence and an end of a sequence and a AAH13629 to AAH13632

AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to

chepsent oligonuclectides, all of which are used in the exemplification

of the full-length cDNAs. all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                            Yamamoto J;
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Yamamoto J;

Saito K, , Otsuki 1

Hayashi K, S. A, Nagai K,

Nishikawa T, Hay T, Wakamatsu A, Nishikawa

Sugiyama

99JP-0248036

2000JP-0241899

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0;
The present invention describes primer sets for synthesising 5602 comprises: (a) an olique-dr primer and an oliquoudleotide complementary to the complementary strand of a polynucleotide which comprises one of a polynucleotide which comprises one of a polynucleotide which comprises one of an oliquoucleotide comprises at least 15 nucleotides; or (b) a combination of an oliquoucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oliquoucleotide comprising a sequence complementary to the polynucleotide which comprises a 3'-end polynucleotide which comprises a 3'-end sequence complementary to a liquoucleotide comprision at least 15 nucleotides and the complementary to a oliquoucleotide comprises a 1'-end sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the S'-end sequence is selected from those defined in in gene therapy. The primer sets can be used in antisense therapy and particularly full-length conservation without soft sets of the abnormality of the proteins encoded by the full-length conservation of the abnormality of the proteins encoded by the full-length conservation in the primers allow obtaining of the full-length conservation in the full-length conservation in the full-length conservation in the full-length without any specialised methods. And set in And 13628 and And 13633 to And 13632 to And 13632 and And 13632 to And 13632 and And 13632 to And 13632 and and 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       474 GTAATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGGCGGAGCCGACCCTTCTCTC 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1556 BP; 380 A; 363 C; 399 G; 414 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.9%; Score 89.4; DB 22; 98.9%; Pred. No. 5.4e-14; Live 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COGGCTGCGCCAGGCCAGGCGGGGACTC 91
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AAH04729 standard; cDNA; 763

AAH04729

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AAH04729;

26-JUN-2001 (first entry)

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligounclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the sequence and an oligonucleotide comprises at least 15 nucleotides and the combination of complementary strand of a polynucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence 3'-end sequence 15 selected from those defined in the specification. The primer sets can be used in antisense therapy and the specification. The primers are useful for synthesising polynucleotides. Particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for AAH13628 and AAH13633 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to Fine and AAH13633 to AAH13632 to AAH13632 to Fine and AAH13633 to AAH13
                                                                          Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saito K, Ya
Otsuki I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 763 32; 137 A; 205 C; 260 G; 158 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID 1564; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashi K,
                        Human cDNA clone (5'-primer) SEQ ID NO:1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                        27-ACG-1999; 994P-0300253:
11-JAN-2000; 2000UP-0118776:
02-MAY-2000; 2000UP-0183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUN-200C; 2000JP-0241899.
                                                                                                                                                                                                                                                                                      2000EP-0115126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suciyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isogai T,
                                                                                                                                                                                EP1074617-A2.
                                                                                                                                                                                                                                                                                      28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAY-2000;
                                                                                                                                 Homo sapiers
                                                                                                                                                                                                                                  07-FEB-2001
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Ishii S,
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AATTGCGAGCGAGAGTGGGGGCGGGACCCGCAGACCGAGCCGACCCTTCTCTCCC 535
                                             Gaps
15.8%; Score 89; DB 22; Length 763;
                                       0; Indels
                    100.0%; Pred. No. 5.6e-14; ive 0; Mismatches 0;
Query Match
Best Local Similarity 100.
Matches 89; Conservative
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0

GGGCTGCGGCAGGGCAGGCGGGGAGCTC 564 536

61

RESULT 14 AAH17451

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dI primer and an oligonucleotide complementary to the complementary strand of a polypurcleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the collegence confides one of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 1'-end sequence, where the oligonucleotide which comprises a 1'-end sequence, sequence of an oligonucleotide sequence and sequence, and an oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence and sequence, and the compination of the sequence and sequence and sequence and polynucleotide of in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length onlyns. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assisy without any specialised methods. AAH13632 to AAH1
                                                                                                                                                                                   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               476 AATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCCC 535
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Otsuki
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A, Nagai X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                        Human cDNA sequence SEQ ID NO:16905
AAH17451 standard; cDNA; 1750 BP.
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100.0%; Pre-
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 20C0JP-0118776.
02-MAY-2000; 20C0JP-0241899.
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                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                            EP1074617-A2
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                                                                                           26-JUN-2001
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Matches 89;
                                             AAH17451;
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GGGCTGCGGCAGGGCAGGGGGGGGGCTC 89

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elaring to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activities activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment of cancer, leukaemia, nervous system disorders, aribritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAK80020) are omitted as the relevant pages from the sequence listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
Yang Y, Wejirman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7281 BP; 1831 A; 1773 C; 1915 G; 1762 T; 0 other;
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Pred. No. 1.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 1086-1096; 6221pp; English.
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                                                                                                                                                                                                                                                                                                                                                                            Human polynucleotide SEQ ID NO 228.
                                                                                                    AAK51683 standard; cDNA; 7281 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000us-0496914.
2000us-0560875.
2000us-0598075.
2000us-0598075.
2000us-0654936.
2000us-0654936.
2000us-0693561.
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86.78;
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                                                                                                                                                                                                                                                                                      (first entry)
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P-PSDB; AAM78550.
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                                                                                                                                                                                          AAK51683;
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AAK51683
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DT O6-NO'
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DO O9-AC
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Human

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Human large AIF-binding cassette transporter 1(hABC1) promoter sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; large AIF-binding cassette transporter 1; ABC1; promoter;
antiarteriosclerotic; gene transfer; transactivator; ds.
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                                                                                                          AAK52667
AAF24680
AAF24702
AAF24685
AAF24685
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AAD37268
AAH07432
AAH18606
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AAK51683
ABA09200
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AAK92108
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AAK94827
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AAH04659
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AAH77797
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AAH15566
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                                                                                    The invention relates to an isolated human large AIP-binding cassette transporter 1 (ABC1) promoter capable of directing transcription of transporter 1s used to be a sequence positioned downstream to it. The hABC1 promoter is useful for expressing foreign DNA in a host ce.1, by introducing into the host cell a gene transfer vector comprising the promoter operably linked to a foreign DNA in a destroop do promoter operably linked to a foreign DNA is expressed. The gene transfer can be introduced into the host cell by adenovirus infection, liposome-mediated transfer, topical application to the cell or microinjection. The gene transfer vector encodes and expresses a reporter molecule. The method further involves introducing into the cell a gene transfer vector comprising a nucleic acid segment encoding a transactivator protein capable of upregulating the ABC1 promoter, or contacting the cell with the transactivator protein, or an agonist of the transactivator protein.
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The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (ATP) binding cassette protein (ABC) i gene. ABC1 resides in cell membranes and utilises ATP Mydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholsterol stores. ABC1 is defective in Tangler disease, a genetic cholsterolise stores. ABC1 is defective in Tangler disease, a genetic choracterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9422-9431. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treamment of and atherosclerosis. The genes associated with hypercholesterolemia and atherosclerosis. The genes associated with hypercholesterolemia to escreen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.
                                                                                                                                                                                                                                                                                                  Adenosine triphosphate (AIP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1532 ACTAGICCCGGCAAAAACCCCGGTAATIGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAG 1591
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100.0%; Pred. No. 3.5e-89;
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                                                                                                                   (CVTH-) CV THERAPBUTICS INC.
                                                                                                                                                                                 Wade D, Garvin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                         WPI; 2001-137812/14.
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Best Local Similarity
Matches 352, Conserv
                                                                                                                                                                                                                                                                                                                                                             and other disord
atherosclerosis
18-JUN-1999;
14-SEP-1999;
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                                                           19-NOV-1999;
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                                                                                                                                                                                 Lawn RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1412
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1532 301

flanking region of the human ABC1

1592 ACCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGCGGGGGAGCTC 1643

QD S

4 09:39:46 2003

Tue Feb

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Adenosine triphosphate (ATP) binding cassette protein (ASC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
                          Human, adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; ciromosome 9922-9931; neart disease; hypercholesterolemia; atheroscierosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                     Disclosure; Page 138-139; 211pp; English.
        Nuclectide sequence of the 5'
                                                                                                                                                          99US-0140264.
                                                                                                                                                                  990S-0153872.
                                                                                                                                      16-JUN-2000; 2000WO-US16591.
                                                                                                                                                                                                  (CVTE-) CV THERAPEUTICS INC.
                                                                                                                                                                                                           (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                 WPI; 2001-137811/14.
                                                                                                                                                                                                                               Wade D,
                                                                                                                                                                                                                                                                                                   atherosclerosis
                                                                                               WC200078971-A2.
                                                                                                                                                          18-JUN-1999;
                                                                                                                                                                     14-SEP-1999;
19-NOV-1999;
                                                                             Homo sapiens
                                                                                                                   28-DEC-2000
                                                                                                                                                                                                                               Lawn RM,
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Garvin M;

Oram JF,

The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangler disease, a genetic and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia to screen for compounds that regulate the expression of genes associate with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia. Sequence 1643 BP; 370 A; 413 C; 457 G; 403 T; 0 other;

.. GAGCACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAATCTATAAAAGGA 240 Gaps .; 0 100.0%; Score 352; DB 22; Length 1643; 100.0%; Pred. No. 3.5e-89; Indels 0 0; Mismatches Conservative il Similarity 352; Conserv Query Match Local Matches 181 g ŎΣ g δď qq ŏ

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selected a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating a lower than normal high density lipoprotein-cholesterol (EDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 ACGIGCTITCTGCTGAGTGACTGAACTACATAAACAGAGGCCGGGAACGGGGCGGGGAGG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 CICCCIAGAIGICICGIGGGGGGCIGAACGICGCCCGTITAAGGGGCGGGCCCCGGCTCC 115
                                                                                                                                                             High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABCl; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABC1 expression or activity. The LXR gene product may be used in an assay to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  compounds useful for the treatment of a disease or condition lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386
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                              ВР
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                              AAF92831 standard; DNA; 183999
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                                                                                                                                                                                                                                                                                                                                                                                          (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                                                           15-MAR-2000; 2000US-0526193.
23-JUN-2000; 2000US-0213958
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                                                                                              (first entry)
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                                                                                                                            Human ABC1 genomic DNA
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Matches 351; Conserv
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AAD37265 RESULT

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2688 CICCCIAGAIGISTSGFGGGGGGGGGGGGGGCGCGTTTAAGGGGGGGGGCCGGSTSC 2747
                                                                                               176 AGGGAGAGCACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAATCTATAA 235
                                                                                                                                        Human, ATP-binding cassette 1, ABC1 gene regulation; atherosclerosis; cholesterol metabolism; hypercholesterolaemia; antisense therapy; ds.
                                                                                                                                                                                                           "LMO2COM/MYOD/DeltaEF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "LMO2COM/MYOD"
                                                                                                                                                                                                                                                                                                                                                                               Human ABC1 transcription regulatory DNA #3.
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/bound_moiety= "S8/NKX2.5"
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708..715
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/bound_mciety= "GATA"
399..410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates a nucleic acid which is capable of regulating the transcription of human APP-binding cassette 1 (ABC1) gene, which is a casual gene for pathologies linked to a dysfunctioning of colosterol metabolism, including diseases such as atherosclerosis. Polynucleotides of the invention are used to screen candidate molecules or substances that are capable of modulating the transcription of the ABC1 gene. They are used in antisense therapy. Compositions comprising sequences of the invention are used to treat inventions are used to treat inventions. The present sequence is human ABC1 transcription regulating DNA.
                                          28644 ACGTGCTTTCTGCTGAGTGACTGAACTACATAAACAGAGGCCGGGAACGGGGCGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid useful for modifying the ATP-binding cassette l (ABCl) and screening for candidate modulatory compounds or substances \,
                          176 AGGGAGAGCACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAATCTATAA 235
                                                                                 Human; ATP-binding cassette i; ABCl gene regulation; atherosclerosis; cholesterol metabolism; hypercholesterolaemia; antisense therapy; ds.
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ey A, Santamarina-Fojo S;
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llarity 98.3%; Pred. No. 1.9e-84;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                       Human ABC1 transcription regulatory DNA #1.
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er N, Remaley A,
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                                                                                                                                                                                                                                    AAD37265 standard; DNA; 3231
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                                                                                                                                                                                                                                                                                           (firs: entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosier-Montus M, Prade
Brewer B, Duverger N,
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                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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Matches 351;
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<pre>21i42152 /*tag= am /bound moiety= "SYR/HFH/HNF3beta"</pre>	4	/bound_molety= "MZF." 22342249 /*tag= ao	/bound_moiety= "IK2/NFkappaB/CREL" 22592272 /*tag= an	/bound_moiety= "LMO2COM/GATA" 22892306 /*+32- 23	50	/ Lay ar /bound_moiety= "PPAR" 2321. 2326	/*tag= as /bound_moiety= "PPAR" 23352342	/*tag= at /bound_moiety= "MZF1" 23612384 /*****	/ ray = au /bound_mclety= "HNF3beta/SRY/EVIl" 24262433	/*tag= av /bound_mojety= "MZF1" 24422451	/*tag= aw /bound_moiety= "AP4" 24552466	/*tag= ax /bound_moiety= "SRY" 24912498	E 23	101	/*tag= ba /bound_moiety= "PPAR" 25892600 /**: bb	/=cg= bb /bcund_mclety= "AP2" 26_0.2617 /*tag= bc	/bound_moiety= "M2Fl" 2634.2648 /*tag= bd	/bound_molety= "LMO2COM/MYOD/E47" 26572672 /*tag= he	/bound_moiety= "RREB1" 2680.2698	/*tag= bi /bound_moiety= "MZF1/CMYB" 27282740	/*tag= bg /bound_moiety= "SP1/GC" 27432757	/*tag= bh /bound_moiety= "JSF/NMYC/ARNT" 27582773	/*tag= bi /bound_moiety= "NFE2AP1" 27742787	/*tag= bj /bound_molety= "XF51/HFH" 27542806
protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein bind	protein_bind
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/bound_molety= "MZF1" 723.730 /*tao= n	/bound_moiety= "MZF1" 771785	/*tag= o /bound_mciety= "HFH2/SRY/EVI1" 803812	= p d_moiety= 837	'NKX2	ety=	ety=	li89:.209 /*ts:.209 /*bound_moiety= "DeltaEF1/LY71/IK2"	ty=	"LMO2-COM/MYOD/del	ety=	ety= "DeltaEF1	1622.162/ /*tag= 2 /bound_moiety= "PPAR"	± 4	li .			E	"AP1		ah noiety= "NKX2.	20062016 /*teg= al ppaR/NXX2.5/PPAR" /Pound_noiety= "PPAR/NXX2.5/PPAR"	"PPAR/NKX2.5/PPAR		21042111 /*tags al /*house "soxs"

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Matches 277; Query Match

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used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, ATP binding cassette transporter 1; ABC1; coronary heart disease; dermatological; atherosclerosis; cardiovascular; inflammatory disease; psoriasis; lipid disorder; antibacterial; septic shock; gene therapy; immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to four common polymorphisms in the gene encoding ATP-binding cassette transporter-1 (ABC1). ABC1 is associated with decreased ApoA-1 mediated efflux of cholesterol. The polymorphisms in ABC1 directly affects cellular lipid homeostasis, which is a key factor in the atherogenetic processes. The ABC1 polymorphisms are useful for diagnosing and treating lipid disorders, cardiovascular diseases
                                                                                                                                                                                                                                                                                                                                                       New adenosine triphosphate binding cassette transporter-1 gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                                                                                                                                                                               1 ATAAAAGGAACTAGTCTCGGCAAAAACCCCGTAATTGCGAGGGGAGAGTGGGGGCCGG
                                                                                                                                                                                                                                                                                                                                  GACCCGCAGAGCCGAGCCGTTCTCTCCGGGGCTGCGGCAGGGCAGGCCGGGGAGCT
                                                                                                                                                      DB 21; Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ATP binding cassette transporter i (ABC1) gene.
                                                                                                                                                    Query Match 33.3%; Score 119.4; DB 21; Best Local Similarity 99.2%; Pred. No. 4.6e-24; Matches 120; Conservative 0; Mismatches 1;
                                                                                                             Seguence 227 BP; 44 A; 65 C; 73 G; 45 I; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Human ABC1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
321..7106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 1; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD21326 standard; DNA; 7260 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAR-2000; 2000EP-0105820.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAE13022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C 121
                                                                                                                                                                                                                                                                                                                                                                                                                        C 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD21326;
                                                                                                                                                                                                                                                                                                                                292
                                                                                                                                                                                                                                                                                                                                                                                                                        352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
AAD21326
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                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTS are derived from mRNAs with intact 5' ends and can therefore be
                                                                                                                                                                                                                                                                                                                                                         2808 AGGAGAGCACAGGCTITGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAATCTATAA 2867
                                                                                                                                                                                                                                               CTCCCTAGATGTGTCGTGGGCGGCTGAACGTCGCCCGTTTAAGGGGGCGCCCCGGCTTC 115
                                                                                                                                                                                                                                                                                                                                                                                                                        176 AGGGAGGCCACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAATCTATAA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                      55
                                                                                                                                                                                2688 CICCCIAGAIGIGIGIGGGCGGCIGAACGICGCCCGIITIAAGGGGGGGGGCCCCGGCTCC
                                                                                                                                                                                                                                                                                                                                  DB 24; Length 2910;
                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2868 AAGGAACTAGTCCGGCAAAAACCCCGTAATTGCGAGGAGAG 2910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 AAGGAACTAGTCCCGGCAAAAACCCCGTAATTGCGAGGGAGAG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein 5' EST, SEQ ID NO: 13690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giordano J;
                                                                 Score 261.4; DB 2
Pred. No. 1.1e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 13690; 71pp + CD-ROM; English.
                       /bound_moiety- "GC/SP1/MZF1"
                                                                                                                 Mismatches
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                                                                   74.38;
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                                                                                                               Conservative
    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI: 2000-500381/45
                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Home sapiens
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Disclosure; Page 26-28; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dp
      .,
(coronary hear: disease, atherosclerosis) and inflammatory diseases (psoriasis, lupus erythematosus). The identification of ABC1 as a transporter for interlevin-lbeta (IL-lbeta) identifies this gene as a candidate for treatment of inflammatory diseases including rheumatoid arthritis and septic shock. The present sequence is human ABC1 gene.
                                                                                                                                                                                                                                                             255 AAACCCCGTAATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCC 314
                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                 1 AAACCCGTAATTGCGAGCGAGAGTGAGTGAGTGAGCCGGGACCCGCAGCCGAGCCGACCC 60
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/note= "alternative open reading frame of AAI70314"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New adenosine triphosphate binding cassette transporter gene polynorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP binding cassette transporter 1; ABC1; human; lipid disorder; coclesterol; cardiovascular disease; inflammatory disease; cartinflammatory; antilipeemic; antipsoriatic; dermatological; Tangier disease; coronary heart disease; diagnosis; gene therapy;
                                                                                                                                                                        Length 7250;
                                                                                                                                                                        27.8%; Score 98; DB 22; Length 726(
106.0%; Pred. No. 1.1e-17;
Live 0; Mismatches 0; Indels
                                                                                                                              Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ATP binding cassette transporter 1 (ABC1) cDNA.
                                                                                                                                                                                                                                                                                                                                               315 TTCTCTCCCGGGCTGCGGCAGGCCAGGGCGGGGAGCTC 352
                                                                                                                                                                                                                                                                                                                                                                   61 TICTCTCCCGGGCTGCGCCAGGCCAGGCGGGGGGGGGGCTC 98
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321..7106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAI70315 standard; cDNA; 7260 BP.
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/*tag= d
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replace(3836,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replace(976, A)
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7:06
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                                                                                                                                                                                                 Best Local Similarity 106. Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polymorphism; ss.
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AAI70315

AAI70315

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triphosphate (ATP) binding cassette transporter 1 (ABC1) protein triphosphate (ATP) binding cassette transporter 1 (ABC1) protein case AMAT50227. The sequence includes an extended open reading frame (ORF) to that provided by the sequence in AAT70314, using an alternative ATG codon as initiation codon and thereby adding an extra 40 N-terminal amino acids to the encoded ABC1 protein (see AAM50228). The invention provides 4 common polymorphisms in the ABC1 gene. These were identified by sequencing the ABC1 gene in AAT70314), G is changed to A at position polymorphisms in the AAT70314, G is changed to A at position 596, T is changed to C at position 136, A is changed to G at position 3456, or any combination of these. ANI of these polymorphisms alter the amino acid sequence of ABC1 and therefore may affect its function. The 2 most common polymorphisms (G596A) and A2589G) are both associated with a decreased in vitro ApoA-1 mediated efflux of cholesterol from monourclear phagocytes, a feature typical of Tangler disease. 3 of the variants (G596A, A2589G and G3456C) are significantly increased in a population of established coronary heart disease. 3 of the variants (G596A, A2589G and G146A) eart for the diseases in a provided ABC1 polymorphisms for the diseases, and inflammatory closeases (CHD) relative to CHD free control subjects. The use of the provided ABC1 polymorphisms for the diseases, and inflammatory closeases (CHD) relative to CHD free control subjects. The use of the provided ABC1 polymorphisms for the diseases, and inflammatory closeases (CHD) relative to CHD free control subjects or ribosyme technology or RNA decoys is also and proper protein by antisense or ribosyme technology or RNA decoys is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 AAACCCCGTAATTGCGAGCGAGAGTGAGTGGGGCCGGGGACCCGCAGGCGGAGCCGAGCCGACCC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; AIP-binding cassette 1; ABCl gene regulation; atherosclerosis; cholesterol metabolism; hypercholesterolaemia; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 7260 BF; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosier-Montus M, Prades C, Lemoine C, Naudin L, Den
Brewer B, Duverger N, Remaley A, Santamarina-Fojo S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; L
i.le-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315 TICTCTCCOGGCTGCGCAGGCAGGCGGGGGGCTC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCTCTCCCGGGCTGCGGCAGGGCAGGGCGGGGAGCTC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1100.0%; Pred. ...
'... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.8%; Score 98; 100.0%; Pred. No.
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es 98; Conserv
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AAH18606;
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AAE18606
ID AAH180
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                                                                                          The invention relates a nucleic acid which is capable of regulating the transcription of human ATP-binding cassette 1 (ABG1) gene, which is a casual gene for pathologies linked to a dysfunctioning of cholesterol metabolism, including diseases such as atherosclerosis. Polynucleotides of the invention are used to screen candidate molecules or substances that are capable of modulating the transcription of the ABC1 gene. They are used to treat hypercholesterolaemia sequences of the invention are used to treat hypercholesterolaemia and atherosclerosis. The present sequence is human ABC1 gene exon lA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                    Isolated nucleic acid useful for modifying the ATP-binding cassette {\tt i} (ABC1) and screening for candidate modulatory compounds or substances
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                                                                                                                                                                                                                                     Score 91, D3 24; Length 221: , Pred. No. 4.3e-16; 0; Mismatches 0; Indels
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Otsuki
                                                                                                                                                                                                             Sequence 221 BP; 44 A; 62 C; 73 G; 42 T; C other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID 4267; 2537pp + CD ROM; English.
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA clone (5'-primer) SEQ ID NO:4257.
                                                                                                                                                                                                                                                                                                                                   322 CCGGGCTGCGGCAGGCAGGCGGGGAGCTC 352
                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 132; 152pp; English.
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T, Wakamatsu
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99JP-0300253.
2000JP-0118776.
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                                                                                                                                                                                                                                                             91; Conservative
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WPI; 2002-154404/20.
                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUN-2000;
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27-AUG-1999;
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Ishii S,
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Sest Local S
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The present invention describes primer sets for synthesising 5602 comprises: (a) an oligo-dT primer and an oligouncheotide comprises: (a) an oligo-dT primer and an oligouncheotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a sequence complementary to the oligonucleotide omprises at least 15 nucleotides and the combination of the 5'-end sequence 27'-end 27'-e
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Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 89.4; DB 22;
Pred. No. 1.6e-15;
C; Mismatches 1;
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 CCGGGCTGCGGCAGGGCAGGGGGGGGGAGCTC 352
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T, Wakamatsu
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0187767.
09-JUN-2000; 2000JP-0187767.
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98.9%;
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Best Local Similarity 98.9
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the present invention
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an obligo-dr primer and an obligonucleotide complementary transfor of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the complementary strand of a polynucleotides; or (b) a combination of a noligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises as 5'-end sequence, and an obligonucleotide comprising a sequence; where the complementary to a polynucleotide which comprises as 3'-end sequence, where the complementary to a polynucleotide comprises at least 15 nucleotides and the combination of the 5°-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the complementary full-length cDNAs. The primers are also useful for the complementary full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH33633 to AAH33633 to AAH33633 to AAH33633 to AAH33633 to AAH33632 to AAH33633 to AAH33630 to AAH33630 to AAH33630 to AAH33630 to AAH336
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   and/or diagnosis of the abnormality of the proteins encoded by the
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                                                                                                           Claim 8; SEQ ID 18808; 2537pp + CD ROM; English.
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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es 90; Conservat
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                                           full-length cONAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comptises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a conjugant comprises a 1-end sequence complementary to a polynucleotide comprises a 1-end sequence where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length. CDNAs. The primers are also useful for the particularly without any specialised methods. AAR03166 to AAR1328 and the cDNAs easily without any specialised methods. AAR03166 to AAR1328 and AAR030303 converses the control of the cDNAs and control of the cDNAs and control of the cDNAs are controlled to the cDNAs are contro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligocucieotides, all of which are used in the exemplification
                                                                      primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 763;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11arity 100.0%; Score 89; DB 22; I 00.0%; Pred. No. 2.1e-15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                      Claim 1; SEQ ID 1564; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 GGGCTGCGGCAGGCCAGGCGGGGAGCTC 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH17451 standard; cDNA; 1750 BP
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99JP-03J0253.
2000JP-0118776.
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0163767.
09-JUN-2000; 2000JP-02418999.
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                     2001-318749/34
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Matches 89; Conserv
                                                                                                                                               full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
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tissue growth factor; immunomodulatory; cancer: leukaemia;
nervous system disorder; arthritis; inflammation; ss.
                                                                Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 2.6e-15;
0; Mismatches 0; Indels
                                                              Saito K, Y. Otsuki I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1750 BP; 291 A; 489 C; 586 G; 384 T; 0 other;
                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID 16905; 2537pp + CD ROM; English.
                                                              Nishikawa T, Hayashi K, S
T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 GGGCIGCGGCAGGCCAGGGGGGGAGCIC 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAK51683 standard; cDNA; 7281 BP
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Matches 89; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the present invention
                    (HELI-) HELIX RES INST
                                                                                                                               WPI; 2001-318749/34.
                                                                                        Sugiyama
                                                                                                                                                                                                                                            full-length cDNAs
                                                              Iscgai T,
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                                                              Ota I, Is
Ishii S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
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Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 AAACCCCGTAATIGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGAGCCGAI4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding polypeptides with cytokine-like activities
                                                                                                                                                                                                                                                                                                                                                                                  Cao Y,
                                                                                                                                                                                                                                                                                                                                                                            Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
Yang Y, Wejhrman I, Goodrich R:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 7281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
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86.7%; Pred. No. 7.5e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 1086-1096; 6221pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful in diagnosis and gene therapy
                                                   20000S-0496914.
2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
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2000US-0693325.
2000US-0728422.
2001WO-US04098
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                                                                                                                                                                                                                                                                                                                        HYSEQ INC.
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05-FEB-2001;
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01-SEP-2000;
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                                                            03-FEB-2000;
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Zhao QA,
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AAL38336 AAI64291 AAC64754 AAH09951

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Macaca mulatta

Human cDNA sequenc Chlamydia pneumoni

AAH17313 ABL91246

143899 1288139 133719 5495 15295 15218 2025 487 1610 32167 4999

AAF80546 AAZ23903 ABN77232 ABA16491 AAQ45913

ABN65684 ABA20621

Human cancer relat

Receptor #34 parti

Human nervous syst Human LO30 homolog

Human ORF2179 cDNA Human nervous syst

DNA encoding novel

Microsatellite mar

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AAH75558
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ABL61947
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AAR76645
AAR10606
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Drosophila melanog

Human reproductive

Human novel protei CDNA sequenc protease PRT ORFX ORF2064

cervical

Human Human Human

AAH14569 ABK12886

AAH68902

1794 5184 18772

6200

206 1981 2185 2185 2189 2317 2317

AAS45130

AAS45131 AAS45132

cDNA encoding n cDNA encoding n cDNA encoding n

ALIGNMENTS

BP.

(first entry)

promoter;

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Human large ATP-binding cassette transporter 1(hABC1) promoter sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiarteriosclerotic; gene
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ABL58400;
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Human RNA-binding
                                                                                             (without alignments)
8245.650 Million cell updates/sec
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                                                                                2003, 12:45:48 ; Search time 37.9628 Seconds
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I gggccccggctccacgtgct.....agccgaatctataaaaggaa 139
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                                                                                                                                                                                                                                                                                                                                       N.Geneseq_101002:*

1. /SIDS2/gggdata/geneseg/genesegr.embl/NA1980.DAT:*

3. /SIDS2/gggdata/geneseg/genesegr.embl/NA1982.DAT:*

3. /SIDS2/gggdata/genesegr.embl/NA1982.DAT:*

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                        Compugen Ltd.
                                                                                                                                                                                                                                   of hits satisfying chosen parameters:
            5.1.3
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                                                                                                                              US-09-596-141C-3_COPY_1394_1532
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             GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                            Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AAD37265
AAF93064
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AAK89398
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AAF24703
AAF92831
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Novel isolated human large AIP-binding cassette transporter I promoter capable of directing transcription of heterologous coding sequence positioned cownstream to it, useful for expressing foreign DNA in bost (JYCO) UNIV COLUMBIA NEW YORK 27-APR-2001; 2001WO-US13654. 28-APR-2000; 2000JS-0560372. WPI; 2002-049334/06. WO200183506-A1. 08-NOV-2001.

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Lawn RM,
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                                                      transporter 1 (ABC1) promoter capable of directing transcription of heterologous coding sequence positioned downstream to it. The hABC1 promoter is useful for expressing foreign DNA in a host cell, by introducing into the host cell a gene transfer vector comprising the promoter operably linked to a foreign DNA according a desired polypeptide or RNA, where the foreign DNA is expressed. The gene transfer can be introduced into the host cell by adenovirus infection, liposome-mediated transfer, topical application to the cell or microinfection. The gene transfer vector encodes and expresses a reporter molecule. The method further involves introducing into the cell or gene transfer vector comprising a nucleic acid segment encoding a transactivator protein capable of upregulating the ABC1 promoter, or contacting the cell with the transactivator protein.
                                                                                                                                                                                                                                                                                                                                                                                      61 CGGGGGGGGGGAGGAGGAGGACAGGCTTTGACGGATAGTAACCTCTGCGCTCGGTGCA 120
                                                invention relates to an isolated human large ATP-binding cassette
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                            1 GGCCCCGGCTCCACGTGCTTTCTGCTGAGTGAACTAAACTAAAAAAAGAGGCCGGGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 flanking region of the human ABC1 gene
                                                                                                                                                                                                                  Modulators of human ABC1 gene expression are useful for treating atheroscierosis. The present sequence represents the hABC1 promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; adenosine triphosphate binding cassette protein 1; ABC1;
apolipoprotein-mediated mobilisation; cholesterol; Tamgier disease;
chromosome 9422-9431; heart disease; hypercholesterolemia;
atherosclerosis; cholesterol transport; ss.
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                                                                                                                                                                                                                                                    Sequence 1197 BP; 284 A; 314 C; 328 G; 271 T; 0 other;
                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide seguence of the 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                               1052 GCCGAATCTATAAAGGAA 1070
                        Claim 1; Fig 3; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wade D, Garvin M;
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                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                    Local Similarity
es 139; Conserv
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19-NOV-1999;
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                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.
Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1394 GGGCCCCGGCTCCACGTGTTCTGCTGAGTGAACTACATAAACAGAGGCCGGGAA 1453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGCCCCGGGCTCCACGTGCTTTCTGCTGAGTGAACTACATAAACAGAGGCCGGGAA 60
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                              useful for the development of agents for the trearment of her
and other disorders associated with hypercholesterolemia and
atherosclerosis
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100.0%; Pred. No. 1.9e-35;
ative 0; Mismatches 0;
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                                                                                                                                                                        Claim 1; Page 143-144; 215pp; English.
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99US-0153872.
99US-0166573.
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Best Local Similarity
Matches 139; Conserv
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19-NOV-1999;
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The present sequence represents the 5' fianking region of the huuman adenosine triphosphate (ATP) binding cassette protein (ABC) I gene. ABCI caesides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABCI is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular choiserrol stores. ABCI is defective in Tangler disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABCI gene is localised to chromosome 9422-9431. The ABCI genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and cother disorders associated with hypercholesterolemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                   Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1394 GGGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAACAGAGGCCGGGAA 1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1454 CGGGCGGGGGGGGGGGGGGGGCAGGCTTTGACCTTTGACCTCTGCGCTCGTGGTGCA 1513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High density lipoprotein-cholesterol; HDL-C: cardiovascular; ABCl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGCCCCGGCTCCACGTGCTTTCTGCTCACTGAACTACATAAACAGAGGCCGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 100.0%; Score 139; DB 22; Length 1543; Local Similarity 100.0%; 2red. No. 1.9e-35; es 139; Conservative 0; Mismatches 0; Indels C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 1643 BP; 370 A; 413 C; 457 G; 403 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pimstone SN, Clee SM;
                                                                                                                                                                                          Disclosure; Page 138-139; 211pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF92831 standard; DNA; 183999 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1514 GCCGAATCTATAAAAGGAA 1532
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23-JUN-2000; 2000US-0213958
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                         2001-137811/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ABC1
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating a lower that normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CEGGGCGGGGAGGAGGAGCACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding cassette 1; ABC1 gene regulation; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cholesterol metabolism; hypercholesterclaemia; antisense therapy; ds.
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                                                                                                                                                                                                                                                               The present invention relates to a method for treating a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 183999;
                                                                                                                                                                                                                                                                           diagnosed as having a lower than normal high density a parky lipoprotein-choiesterol (HDL-C) level, a higher than normal trigiveride level, or a cardiovascular disease, involving administering a compound that modulates LNR- or RNR-mediated transcriptional activity or ABC1 expression or activity. The LNR gene product may be used in an assay to identify compounds useful for the treatment of a disease or conditions lower than normal HDL cholesterol level, a higher than normal trigilyceride level, and a cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 139; DB 22;
llarity 100.0%; Pred. No. 7.5e-35;
Conservative 0: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /bound_moiety= "LMG2COM/MYOD"
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/bound_moiety= "58"
228..237
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                                                                                                                                                                                                     Claim 8; Fig 1; 317pp; English.
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WPI; 2001-244356/25
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Matches 139; Conserv
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protein_bind	protein_bind	protein_bind	procein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind	protein_bind
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ty= "TK2"	ty= "LYF1"	ty= "LMO2COM/MYOD/Del	ty= "LY31"	ty= "DeltaEF1"	ty= "LKX2.5"	ty~ "NFY/CAA?"	ty= "MZF1"	Ly= "MZF1"	ty= "HFH2/SRY/EVIl"	ty= "CREBP1/VBP"	ty= "NKX2.5"	ty= "GATA"	ty= "LXRalpha/deltaEF1"	ty= "Delta3F1/LYF1/IK2"	cy= "AP4"	ty= "LMO2-COM/MYOD/deltaEF1/E47"	ty= "ZID/deltaEF1"	ty= "DeltaE71"	ty= "ppA3"	ty= "ppar"	ty= "USF/NMYC/MYCMAX"	sty= "DeltaE?1"	ety= "DeltaBFl"	ty= "SRY"
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The invention relates a nucleic acid which is capable of regulating the transcription of human AIP-binding cassette 1 (ABC1) gene, which is a casual gene for pathologies linked to a dysfunctioning of cholesterol metabolism, including diseases such as atherosclerosis. Polynucleotides of the invention are used to screen candidate molecules or substances of that are capable of modulating the transcription of the ABC1 gene. They are used in antisense therapy. Compositions comprising sequences of the invention are used to treat hypercholesterolaemia and atherosclerosis. The present sequence is human ABC1 transcription regulating DNA.
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                                                                                                                                                                                                                                                                          2735 GGGCCCCGGCTCCACGTGCTTCTGCTGAGTGAACTACATAAACAGAGCCGGGAA 2794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds
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                                                                                                                                                                                                        Query Match 98.8%; Score 137.4; DB 24; Length 3231; Best Local Similarity 99.3%; Pred. No. 7.8e-35; Matches 138; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                Sequence 3231 BP; 809 A; 773 C; 876 G; 773 T; 0 other;
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                          Claim 1; Page 130-131; 152pp; English.
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15-MAR-2000; 2000US-0526193.
23-JUN-2000; 2000US-0213958.
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                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid useful for modifying the ATP-binding cassette 1 (ABC1) and screening for candidate modulatory compounds or substances \,
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                                                                                                                                                                                                                                                                                                                                                              1 GGGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAACAGAGGCCGGGAA 60
                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                             Length 2910;
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ley A, Santamarína-Fojo S;
                                                                                                                                                                                                                                                                                                             24;
             "LMO2COM/MYOD/E47"
                                                                                                                                                                                                                                                                                                            Score 137.4; DB 2 Pred. No. 7.6e-35;
                                                                                                                                                                    "USF/NMYC/ARNT"
                                                                                                                                                                                                                                                                                  /bound_moiety= "GC/SP1/MZF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ABC1 transcription regulatory DNA #1.
                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                       "MZF1/CMYB"
                                                                                                                                                                                                                                              "XFD1/HEH"
                                                                                                                                                                                                        "NFE2AP1"
                                                                                                                           "SP1/GC"
                                                   "RREB1"
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Prover R. Duverger N, Remaley A,
                                                                        /*tag= bf
/bound_moiety= "
2728..2740
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/bound_moiety= "
2743..2757
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2680..2698
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2758..2773
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99.3%;
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                                                                                                                                                                                                                                                                                                                         Local Similarity
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14-AUG-2000;
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         trigiveride level, or a cardiovascular disease, involving administering a compound that modulates LNR- or RNR-mediated transfering a compound that modulates LNR- or RNR-mediated transfering a compound and sectivity or ABC1 expression or activity. In LNR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected a lower than normal BDL choles-erol level, a higher than normal trigilyceride level, and a cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid sequence encoding RNA-binding polypeptide ZRPI - useful to reduce angiogenesis, increase cell proliferation or kidney cell regeneration or inhibit tumour growth
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         confactivated receptors (e.g. EGF and PDGR receptors) and specifically bind small nucleotar NASs (e.g. U3). Saccharomyces cerevisiae, Schizosaccharomyces pombe and human ERRI clones (see AAV04062-64) were identified using a mouse ERPI clone (see AAV04061) as probe. The isolated clones can be expressed in the usual host cells. ZPRI is expressed at an elevated level in tumour derived cells, and is a marker for growth and differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This nucleotide sequence comprises a cDNA clone coding for human 2XP1 (see AAW38457), a protein that belongs to a novel class of signalling molecules (see also AAW38454-57) that bind to
                                                                                                                                                                                                                                                                                                                                                                    2PRI; RNA-binding protein; non-activated receptor complex; human; signal transduction; epidermal growth factor receptor; platelet derived growth factor receptor; cancer; tumour; marker; angigenesis; diabetic retinopathy; rheumatoid arthritis; psoriasis; coronary atheroma; renal failure; gene therapy; ss.
                                                                                                                                                           0;
                                                                                                                                   Length 38;
                                                                                                                                                           Indels
                                                                                                                                   26.2%; Score 36.4; DB 22; 97.4%; Pred. No. 0.018; Live 0; Mismatches 1;
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                                                                                                                                                                                                | CTGCTGAGTGACTACATAAACAGAGGCCGGGTA 38
                                                                                                           Sequence 38 BP; 12 A; 8 C; 11 G; 7 T; 0 other;
                                                                                                                                                                                    23 CTGCTGAGTGACTGAACTACATAAACAGAGGCCGGGAA
 (HDL-C) level, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
29..1408
/*tag= a
                                                                                                                                                                                                                                                                                                                                                Human RNA-binding protein ZPR1 cDNA.
                                                                                                                                                                                                                                                                       AAV04064 standard; cDNA; 1817 BP
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                                                                                                                                                             Conservative
 lipoprotein-cholesterol
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                                                                                                                                                Local Similarity
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processes, including malignant transformation of cells. ZPR1, optionally expressed by gene therapy methods, can be used to inhibit the prollferation of ZPR1 associated malignant cells, or for the detection of ZPR1 suppressors and modulators of ZPR1 gene expression. Suppressors increase cell prollferation, reduce anglogenesis, e.g. to treat tumours, diabetic retinopathy, rheumatoid arthritis, psoriasis and coronary atheroma, and/or increase tubular regeneration of kidney cells, e.g. following acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human digestive system antigen genomic sequence SEQ ID NO: 2974.
                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                       Length 1817;
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Pred. No. 6.5;
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61.5%;
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200005-0205515.
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Best Local Similarity
Matches 48; Conserv
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                                                                                                                                                                                      renal failure.
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17-MAR-2000;
18-APR-2000;
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14-AUG-2000;
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14-AUG-2000; 2000US-0225447.

14-AUG-2000; 2000US-0225759.

14-AUG-2000; 2000US-0225759.

18-AUG-2000; 2000US-0225759.

18-AUG-2000; 2000US-0225759.

22-AUG-2000; 2000US-02268681.

22-AUG-2000; 2000US-02268681.

22-AUG-2000; 2000US-0226924.

01-SEP-2000; 2000US-0229344.

01-SEP-2000; 2000US-0229345.

02-SEP-2000; 2000US-0229345.

03-SEP-2000; 2000US-0229345.

04-SEP-2000; 2000US-0229345.

06-SEP-2000; 2000US-023945.

06-SEP-2000; 2000US-023945.

06-SEP-2000; 2000US-023945.

06-SEP-2000; 2000US-023945.

06-SEP-2000; 2000US-023945.

06-SEP-2000; 2000US-023946.

14-SEP-2000; 2000US-0233061.

15-SEP-2000; 2000US-0233061.

16-SEP-2000; 2000US-0233061.

17-SEP-2000; 2000US-0233061.

18-SEP-2000; 2000US-0233061.

19-SEP-2000; 2000US-0233061.

20-SEP-2000; 2000US-0233061.

20-SEP-200
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1 GGGCCCCGGCTCCACGTGCTTTCTGCTGACTGAACTACATAAACAGAGGCCGGGAA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of digestive system, particularly cancer and cancer metastases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.6%; Score 30; DB 22; Length 5868; 61.5%; Pred. No. 9;
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06-DEC-2000, 200005-0251479.
08-DEC-2000, 200005-0251866.
08-DEC-2000, 200005-0251869.
08-DEC-2000, 200005-0251869.
08-DEC-2000, 200005-0251989.
08-DEC-2000, 200005-0251989.
08-DEC-2000, 200005-0251989.
08-DEC-2000, 200005-0251989.
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20000S-0249207.
20000S-0249210.
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20000S-0249210.
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2000US-0250160.
2000US-0250391.
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2000US-0251988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-502630/55
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08-NOV-2000; 208-NOV-2000; 208-NOV-2000; 208-NOV-2000; 208-NOV-2000; 217-NOV-2000; 217
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01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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L7-NOV-2000;
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200CUS-0249212.
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20000S-0249218.
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2000US-0246532.
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2000US-0241809.
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2000US-0244617
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17 - NOV - 2006;
17 - NOV - 2006;
17 - NOV - 2000;
12 - SEP - 2000; 2 14 - SEP - 2000; 2 15 - SEP - 2000; 2 25 - SEP - 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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08-NOV-2000)
08-NOV-2000)
08-NOV-2000)
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01-DEC-2000;
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-NOV-2000;
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17-NOV-2000;
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     Human; digestive system antigen; gene therapy; cancer; appendicitis; ulcerative colitis; infection; Hirschsprung's disease; chronic colitis; digestive system disorder; Meckel's diverticulum; ds.
                                                                                                                                             Human digestive system antigen genomic sequence SEQ ID NO: 2975.
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                                                                                                                                                                                                                                                                                                                                                                                 31. JAN-2000; 2000US-0179065.

24 FEB-2000; 2000US-01186464.

02 MARR-2000; 2000US-01186550.

16 MAR-2000; 2000US-01186350.

16 MAR-2000; 2000US-0118135.

17 MAR-2000; 2000US-0129113.

18 ARR-2000; 2000US-0129113.

19 MAY-2000; 2000US-0129113.

19 JUN-2000; 2000US-0121886.

20 JUN-2000; 2000US-0121886.

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11 JUL-2000; 2000US-0121886.

14 JUL-2000; 2000US-0121886.

14 AUG-2000; 2000US-01225214.

14 AUG-2000; 2000US-0125214.

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16 AUG-2000; 2000US-0125214.

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10 SEP-2000; 2000US-012914.

11 SEP-2000; 2000US-012914.

11 SEP-2000; 2000US-012914.

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17 SEP-2000; 2000US-012914.

18 SEP-2000; 2000US-012914.
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08-SEP-2000; 2000US-0232081
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00005-0232080
                                                                                                                                                                                                                                                                                                                                                       17-JAN-2001; 2001WO-US01324
                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                    W0200155314-A2
                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                          05-NOV-2001
                                                                                                                                                                                                                                                                                                                       02-AUG-2001
                                                                          AAK89399;
         RESULT 10
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base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "biallelic marker 20-841-149, polymorphic base A or G" replace(45442,A,G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polymorphic
                                                                                                                                                                                                                                                                                                                                                      /note= "biallelic marker 17-42-315, polymorphic base C or I"
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replace(77058,C,T)
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complement (12581..12603)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (15460..15482)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (1357..1377)
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                                                                                                                                                                                                                                                                                                                                                                                 replace(15241,C,T)
                                                                                                                                                                                                                                                                          replace(1239, C, T)
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/number= 2
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                              /number=
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                                                                                                                           exon
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                                              uoxe
     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of a number of auman digestive system antiques. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic. Infections, appendictis, Hitschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAACAGAGGCCGGGAA 60
                                                                                                                                                                                                                                                        Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing discrders of the digestive system, particularly cancer and cancer metaszases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apolipoprotein A-IV-related protein, AA4RP; human;
biallelic marker; lipid metabolism; liver related disorder;
obesity; dlabetes; coronary heart disease; diagnosis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.6%; Score 30; DB 22; Length 10316; 61.5%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10316 BP; 2525 A; 2093 C; 2534 G; 3164 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30; Indels
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                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 2975; 986pp; English
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08-DEC-2000; 2000US-0251969.
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12947..12958
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                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
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/number= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CGGGGCGGGGGGGGA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 CGGGGCCGGGGGGGA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                               WPI; 2001-502630/55.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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5'UTR
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Matches
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AAF30035/0
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complement (77166..77185)
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note= "20-828-311 probe'
                                                                                                                                                                                                                                                                                                                                                                                                                                        aq
"17-41-250 probe"
                                                                                                                                                                                                                                                                                                                                                                                                                    "17-42-319 probe'
                                                                                     complement (1240..1258)
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/note= "20-842-115
77046..77070
                    /*tag= aa
/note= "primer
                                                                                                                                                                   ..15240
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99WO-IB02058.
99US-0469099.
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                                                              .1238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_binding
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                                                                                                                                                                                                                                                                                               primer_bind
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          primer_bind
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Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal, nephrocropic; antilnfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative discade; wound; infectious disease; ss.
                                                                                                                                                                                                                                                                         The present sequence is that of the human apolipoprotein
A-IV-related protein (AA4RP) gene on chromosome 11. The gene
encodes a $66-amino acid protein (see AAB20103). AA4RP is
clifferentially expressed in obese mouse models, indicating a role
in lipid metabolism related disorders. It appears to be the human
composition of a regeneration associated protein (RA43), which is
believed to be involved in liver regeneration, and is likely to
have a similar function. It also shows 52% similarity to
apolipoprotein A-IV, and is likely to have a similar function. The
invention also provides AA4RP coNAS (see AAF30036) and polypeptides,
bialialic markers identified in the AA4RP gene and from genomic
regions flanking the gene, and methods for genotyping a nucleic
card containing 1 or more of the biallelic markers. Also provided
is a method for detecting a statistical correlation between a
biallelic marker allele and a phenotype and/or between a biallelic
marker mathod provided and phenotype and stream and provided
for an are provided and phenotype and a phenotype and such or an entitle of an entitle of the property of a present of the provided of the property of a phenotype and a phenotype and a phenotype and a phenotype and a method for detecting a statistical correlation between a biallelic
                                                                                                                                             Nucleic acids encoding apolipoprotein A-IV-related proteins (AA4RP) and bialielic markers of AA4RP, useful for diagnosing lipid metabolism related disorders and/or liver related disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17479 GGCCTGCTCCTCGTCGTCCTCGGCGCTGATGGCCGGAACAGGTGATCAGGGGCAGGCG 17420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTACATAAAACAGAGGCCGGGAA 60
                Duclert A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for determining whether an individual is at risk of developing a lipid metabolism related disorder and/or a liver related disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate cancer antigen nucleotide sequence SEQ ID NO:320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 81001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30; Indels
                Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 22:
Pred. No. 19;
0; Mismatches 30;
                Bihain B,
                                                                                                                                                                                                                                        Claim 1; Page 216-238; 260pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
AAF15885/c
ID AAF15885 standard; cDNA; 1756 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17419 cesecceseccesces 17402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 61.5%;
Matches 48; Conservative C
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                  Bour B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGGGGGGGGGGGGA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                  Yen F, Demison B, Bo
Dumas Milne Edwards J;
                                                                                 WPI; 2001-071485/08
                                                                                                        P-PSDB; AAB20103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200055174-A1.
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(HUMA-) HUMAN GENOME SCI INC.

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monophasic demyelination; encephalomyelitis; Marchiafava-Bignami disease;
                                                                                                                                                                                                                                               AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB5533 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polyunclectides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cerebroprotective, geuroprotective, cytostatic, Nogo receptor homologue, NGR2; NGR3; axonal growth, central nervous system; CNS; cerebral injury; spinal cord injury; stroke; demyelinating disease; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                           disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF1656 to AAF16514 to AAF57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                       research purposes. The prostate cancer antigens may be used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multifocal leukoencephalopathy; panencephalitis; Spongy degeneration; Alexander's disease; Canavar's disease; Canavar's disease; Krabbe's disease; immune; bait protein; genetic mapping; gene therapy; transgenic animal; unregulated cellular growth; cancer; tumour; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTGAAACATAAACAGAGGCCGGGAA 60
                                                                                                                                 te cancer associated gene sequences, referred to as prostate antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 29.6; DB 21; Length 1756;
Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1756 BP; 447 A; 447 C; 481 G; 369 T; 12 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic sequence encoding a human NgR2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                          disorders such as prostate cancer -
                                                                                                                                                                                                                Claim 1; Page 829; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAL38336 standard; DNA; 143899 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.3%;
L Similarity 60.3%;
47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                        Rosen CA, Ruben SM;
                                                                           2000-587513/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query March
Best Local Similarity
(ROSE/) ROSEN C A.
                                                                                                 P-PSDB; AAB56682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAL38336;
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The invention relates to a Nogo receptor homologue polypeptide, NGR2 or NGR3, comprising a 50 amino acid LRRCT sequence, a 284 amino acid NTLRRCT sequence, all given in the sequence, or a 420, 461 or 392 amino acid sequence, all given in the specification. The NGR3 protein or its binding antibody is useful for specification. The NGR3 protein or its binding antibody is useful for centron, by contracting the neuron NGR3 or its antibody, and for treating contracting the neuron NGR3 or its antibody, and for treating corphality. Spinal cord injury, stroke, comprehensive in a vector comprising NGR3 is useful for treating cerebral injury, spinal cord injury, stroke, panencephalitis, Marchiafava-Bignami disease, Spongy degeneration, campanal dagalest sease, nettachomatic leukokystrophy and knexabe's disease, Camavan's disease, Spongy degeneration, campanal dagainst NGR3, as a bait protein in a two-hybrid or three-hybrid cassay, and as a research tool for identification, threaterisation and purification of interacting, regulatory proteins. The nucleotide sequences of the invention are useful for screening for RFIP associated with cartaining NGR3 is useful for producing non-human transgenic animals. The NGR8 binding antibody is useful for isolating and purifying and the invention and/or quantization of MGR3, and for derephence of NGR3, is useful for isolating and purifying and the hyperic numbers of the invention and/or quantization of hisolating with a second campanal containing NGR3 is useful for producing non-human transgenic animals. The NGR8 binding antibody is useful for isolating and purifying and the hypersonic manner the second of the invention and/or quantization of hisolating and purifying and the hypersonic manner when the hypersonic and the hypersonic animals. The NGR8 binding antibody is useful for invention and purifying and purifying and purifying and hypersonic manner when the hypersonic animals in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 123799 GGGCGCTAGAAAGAGGATAGTTCTACTGATTGAGTGACAGATAAGGGTGTGGGCCAGAGA 123858
                                                                                                                                                                                                 Novel Nogo receptor homolog polypeptide, NgR2 or NgR3, useful for treating central nervous system disorder, cerebral injury, spinal cord injury, stroke, and demyelinating diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and therapeutic purposes. The sequences of the invention, vectors and antibodies are useful for treating or preventing unrequiated callular growth such as cancer and tumour growth. This polynucleotide sequence represents the genomic sequence encoding a human NgR2 protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRV; rhesus rhadinovirus; japanese macaque virus; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTACATAAACAGAGGCCGGGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 143899 BP; 36346 A; 35277 C; 35318 G; 35657 T; 1301 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.2%: Score 29.4; DB 24; Length 143899; 55.3%: Pred. No. 35; 1.0e 0; Mismatches 46; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JMNN. cytostatic; antiasthmatic; antiallergic; dermatological; vulnerary; gene therapy; leucopenia; thrombocytopaenia; inflammatory disease; asthma; allergy; dermatitis; virus; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 123859 CTGGGGGTGGGGAGGGTCAGGGGAGAGGATAGGAA 123901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CGGGGCGGGGAGGGAGGCACACAGCCTTTGACCGATAGTAA 103
                                                                                                                                                                                                                                                                                                                             Example 2; Page 176-214; 277pp; English.
                                                                                         Sah DWY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca mulatta rhadinovirus 17577
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                                                                                      RL,
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Best Local Similarity 55.3'
Matches 57; Conservative
                                                                                            Cate
                              ) BIOGEN INC
(UYYA ) UNIV YALE.
(BIOJ ) BIOGEN INC
                                                                                         Strittmatter SM,
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Gaps

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Location/Qualifiers

Key

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labėl= RRV_ORF29a
/note= "has similarity to KSEV ORF29a"
                                                                                                                                                                                                                                /*tag~ v /product= "major capsid protein" /label= RRV_ORF25 /note= "has similarity to KSHV ORF25" 43491...44408
                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= z
/label= RRV_ORF29b
//note= "has similarity to KSHV ORF29b'
46905..47135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= RRV_CRF35
/note= "has similarity to XSHV ORF35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= ab
/label= RRV_ORF31
/note= "has similarity to XSHV ORF31"
47683..49077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= RRV_ORF34
/note= "has similarity to KSHV ORF34"
51923..52372
                                                                                                       /*tag= s /*tag= sglycoprotein H" /products /21/20 //probl= RRV_ORF22 //octe= "has similarity to KSHV ORF22" complement (35865..37073)
                                                                                                                                                                                                                                                                                   /product "capsid protein"
/Jabel= RRV_ORP26
/note= "has similarity to KSHV ORP26"
44433..45242
/note= "has similarity to KSHV ORF19"
complement (31043..32095)
                                                                                                                                                                                                                                                                                                                                                                                      /note= "has_similarity to KSHV ORF28"
complement (45733..46779)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "has similarity to KSHV ORF32"
49049..50059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "has similarity to KSHV ORF33"
complement (49977..50960)
                   /*tag= q
/label= RRV_ORP20
/note= "has similarity to KSHV ORF20"
32094..33767
                                                                /oroduct= "thymidine kinase"
/label= RRV_CRF21
//note= "has similarity to KSHV ORF21"
33754..35868
                                                                                                                                                              /label= RRV_ORF23
/note= "has similarity to KSHV ORF23"
complement (37123..39321)
                                                                                                                                                                                                              /note= "has similarity to KSHV ORF24"
39323..43459
                                                                                                                                                                                                                                                                                                                                                 /note= "has similarity to KSHV ORF27"
15408..45683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                to KSHV ORF30*
                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= aa
/label= RRV_ORF30
/note= "has similarity
47093..47746
                                                                                                                                                                                                                                                                                                                                                                     /*tag= y
/label= RRV_ORF28
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'label= RRV_ORF33
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'label= RRV_ORF32
                                                                                                                                                                                                                                                                                                                               /*tag= x
/label= RRV_ORF27
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/label= RRV_ORF24
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/nois= "has similarity to Kaposi's sarcoma-associated
virus (KSHV) open reading frame (ORF) 2"
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lymphoproliferative disorder; B-cell hyperplasia; lymphadenopathy;
splenomegaly; hypergammaglobinulinaemia; autoimmune haemolytic anaemia;
                                                                                                                                                                                                                                                                                                                                                                                            Macaca mulatta rhadinovirus 17577; RRV; rhesus macaque rhadinovirus; genome; Kaposi's sarcoma-associated herpesvirus; KSHV; interleukin 6; LL-6; macrophage inflammatory protein; MIP; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                   10 CTCCACGTGCITTCIGCTGAGTGACTGAACTACATAAACAGGGCGGGGAACGGGGCGGG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca mulatta rhadinovirus 17577 (RRV) genome sequence SEQ ID NO:1.
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                                                                                                                                                                                                                                                                                                                               /note= "has similarity to KSHV ORF43"
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                                                                                                                                                           ORF39'
                                                                                                                                                                                                                                                                                                                                                 DB 24;
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complement (59297..61027)
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                                                                                                                                                                                                                               "helicase/primase"
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                                                                                                                                         "giycoprotein M"
                                                                                                                                                                                                                                                                                                             /product= "capsid protein"
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                "kinase"
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                         /label= RRV_ORF36
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54.8%;
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The present invention describes a novel rhesus macaque rhadinovirus called macaca mulatta rhadinovirus 17377 (RRV). AAC64754 represents the groups esquence, and AAB53123 to AAB53204 represent the proteins encoded by the genome sequence. The present invention also specifically claims the individual open reading frame (ORF) nucleotide sequences from the genome which encode the individual proteins, but these sequences are not given. A non-human animal infected with RRV can be used for testing the efficacy of drug in the treatment of condition associated with infection with RRV such as Kaposi's sarroma, impopronificative infection with RRV such as Kaposi's sarroma, impopronificative disorders, B-cell hyperplasia, lymphodenopathy, splenomegaly, hypergammaglobinulinaemia or autoimmune haemolytic anaemia, by administering the drug to a immuno-compromised non-human primate model for testing potential treatments for conditions by Simian Immunodeficiency Virus (SIV). RRV is useful for producing non-human primate model for testing potential treatments for conditions associated with its infection it is also useful for testing the effect capable of infection with RRV incoulating the subject with RRV and observing the effect of vaccine. Asc64755 and AAB53205 to AAB53213 represent sequence used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                    New thesus rhadino virus for producing non-human primate model useful for testing potential treatments and efficacy of the candidate vaccine for conditions associated with RRV infection .
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Pred. No. 54;
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                                                                                                                                                                                                                                                           Searles RP;
                                                                                                                                                                                  (UYOR-) UNIV OREGON HEALTH SCI.
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Matches 57; Conserv
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   1666E-AON-90
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Copyright (c) 1993 - 2003 Compugen Ltd.
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SUMMARIES

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Result		Query				
NO.	Score	Match	Length	DB	QH	Description
_	547.4	97.I	3231	10	US-09-846-456-1	Sequence 1, Appli
2	56.	80.9	2893	10	US-09-846-456-3	
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c 31	35.6	6.3	1797	10	US-09-834-975-987	987, A
c 32			1797	10	US-09-834-975-1003	1003,
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C 14		6.3	1797	10	US-09-834-975-1024	
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25 OY OY OY

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10	RESULT 1 US-09-846-456-1 Sequence 1, Application US/09846456 Patent No. US20020146792A1 SEQUENCE 1, Papilication US/09846456 Patent No. US20020146792A1 SEQUENCE 1 Profer Warie APPLICANT: Profer Warie APPLICANT: Denofice Cendrine APPLICANT: Denofice Patrice APPLICANT: Profer Patrice APPLICANT: NUMBER: US/09/946,455 CUBRENT FILING DATE: 2001-05-02 PRIOR FILING DATE: 2001-05-02 PRIOR FILING DATE: 2001-05-02 PRIOR FILING DATE: 2001-05-02 PRIOR FILING DATE: 2001-05-02 NUMBER OF SED ID NOS: 20 SEQ ID NOS: 20 SEQ ID NOS: 20 SEQ ID NOS: 20 SEQ ID NOS: 30 SEQ ID NOS: 31 TITLE DENOFILE SET SET SET SET SET SET SET SET SET SE	tch sal Similarity 98.9%, Pred. No. 3e-140; 563; Conservative 0; Mismatches 1; Indels 5; Gaps 1; GAGCTCTCTCCCCCAATCCCTCCGGCTGAGGAACTAACAAAGGAAAAAAAA
119884 66.11 119884 66.11 119884 66.11 119884 66.00 66	RESULI 1 US-39-846-456-1 Sequence 1, Application US/C GENERAL INFORMATION: PATENT NO. US20COL16792A1 APPLICANT: Roaler, Marie APPLICANT: Lemoine, Laurent APPLICANT: Denefie, Partic APPLICANT: Bewer, Bryan APPLICANT: Remaley, Alan APPLICANT: For INVENTION: Regulat; TITLE OF INVENTION: Selviat TITLE OF INVENTION: Selviat FILE REPERENCE: 3806.0505 CURRENT APPLICATION NUMBER: CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2001- PRIOR FILING DATE: 2000-05- NUMBER OF SEQ ID NOS: 20 SEQ ID NO 1 LENGTH: 3231 TYPE: DNA US-09-846-456-1	Similarity 98.9%; 63; Conservative GCTCTCTCCCCCAATCCCGAATCCCGAATCCCGCCAATCCCGCCAATCCCGCCCAATCCCGCCCAATCCCAATCCCCAATCCCAATCCCCCCAATCCCAATCCCAATCCCCAATCCCCCAATCCCCCC
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APPLICANT: Lemoine, Cendrine
APPLICANT: Naudin, Laurent
APPLICANT: Denefile, Patrice
APPLICANT: Denefile, Patrice
APPLICANT: Brewer, Bryan
APPLICANT: Remaley, Alan
APPLICANT: Requiatory Nucleic Acid for the ABCI Gene, Molecules Modifying
TITLE OF INVENTION: Activity and Therapeutic Uses
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                                                                                                                                                                              2656 ACCCCCACCCACCCACCCACCACCACCCCAAAOTCCCTAGATGTGTGTGGGCGGCTGAA
  121 GGACTAGAGAGTCTGCGGCGCAGCCCCGAGCGCTTCCCGGGGGTCTTAGGCCGGC
                                                                                                                                                         296 CGTCGCCCGTITAAGGGGCCGGGCCCCGGCTCCACGTGCTTTCTGCTGAGTGACTA
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6.le-16;
hes 0;
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CURRENT APPLICATION NUMBER: US/09/846,456
CURRENT FILING DATE: 2001-05-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09846456
Patent No. US20020146792A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: YAN, Chunhua et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosier, Marie
APPLICANT: Prades, Catherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.0
es 91; Conservative
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Matches
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APPLICANT: Brewar: Bryan
APPLICANT: Remaley, Alan
APPLICANT: Fojo, Silvia
APPLICANT: Fojo, Silvia
APPLICANT: Fojo, Silvia
APPLICANT: Remaley, Nucleic Acid for the ABC1 Gene, Kolecules Modifying It
IITLE OF INVENTION: Activity and Therapeutic Uses
FILE REPERENCE: 3806.0505
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                                                                                                                                                                                                                                                                                                                   2536 GGACTAGAGAGTCTGCGGGGGGGGGGGGGGCTTCCGGGGGCTTTAGGGCGGG
                                                        GGGCCCGGGCGGGAAGGGGACGCAGACGCGGGACCCTAAGACACTGCTGCTGCTCCTCC
                                                                                               2596 GGGCCGGGCGGGGAAGGGACGCAGACCGCGACCCTAAGACACCTGCTGTACCCTCC
                                                                                                                                  241 AC----CCCCACCCACCCACCTCCCCCAACTCCTAGATGTGTGTGGGCGGCTGAA
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Pred. No. 2.1e-115;
0; Mismatches 1; 1
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CURRENT FILING DATE: 2001-05-02
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PRIOR APPLICATION NUMBER: CS 60/201,280
PRIOR FILING DATE: 2000-05-02
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Patent No. US20020146792a1
GENERAL INFORMATION:
APPLICANT: Rosier: Marie
APPLICANT: Prades, Catherine
APPLICANT: Lemoine, Cendrine
APPLICANT: Lemoine, Lemoine, Cendrine
APPLICANT: Denefle, Fatrice
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SOFTWARE: Patentin version 3.0
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US-09-846-456-3
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Sequence 3, Application US/09815048
Patent No. US20020137131A1
GENERAL INFORMATION:
APPLICANT: W3I, Ming-Hui et al.
APPLICANT: W3I, Ming-Hui et al.
TITLE OF INVENTION: ISCLATED HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL601180
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TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PRCTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCOSING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
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1.7;
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                                                                                                                                                                                                                                                                               0; Mismatches
                                                 FILE REFERENCE: CL001079
CURRENT APPLICATION NUMBER: US/09/770,689A
CURRENT FILING DAIE: 2001-01-29
NUMBER OF SEO ID NOS: 5
SOFTWARE: FASELSEQ for Windows Version 4.0
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CUBRENT FILING DATE: 2011-03-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No.
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Thes 74; Conservative
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Matches 86; Conserve
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US-09-815-048-3
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US-09-770-689A-3
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US-09-815-048-3
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APPLICANT: LARRICK, JAMES W.
APPLICANT: WYORF, KEITH L.
TILLE OF INVENTION: NOVEL INJUDABLESINS FOR TREATING AND PREVENTING VIRAL
TILLE OF INVENTION: AND SACTERIAL DISEASES
FILE REFERENCE: 030905.0004.CIP1
CURRENT APPLICATION NUMBER: US/10/047.542
CURRENT APPLICATION NUMBER: US/10/047.542
FRIOR APPLICATION NUMBER: PCI/US01/13932
PRIOR FILING DATE: 2001-04-28
PRIOR FILING DATE: 2001-04-28
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
SOFTWARE PATENTION NUMBER: 60/200,298
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 400-04-28
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 400-04-28
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Szalay, Aladar
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267
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Pred. No. 0.67;
0; Mismatches 98; Indels 0
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,462A
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FILING DATE: 15-JUL-1996
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APPLICATION NUMBER: 08/835,682
FILING DATE: 10-APR-1997
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FILING DATE: 07-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 10-Sep-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 49.5%;
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: La Jolla
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TYPE: DNA
ORGANISM: Homo sapiens
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US-09-772-304A-1
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hadlaczky, Gyula
TIILE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES IHEREOF AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jength 42999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOR PREPARING ARTIFICIAL CHROMOSOMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
CARRESSEE: Heller Erman Waire & McAwliffe LLP
STREET: 4350 La Jolla Village Drive, 7th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 CCCICCACCCCACCCCACCTCCCCCCCAACTCCCTAGA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 51.9%; Score 37.2; DB 9; Similarity 51.9%; Pred. No. 2.1; 34; Conservative 0; Mismarches 77
                                               TELEFAX: 858-587-5360
TELEFAX: 858-587-5360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/125,767
FILING DATE: 17-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/724,693
FILING DATE: 28-NCV-2000
APPLICATION NUMBER: 08/835,682
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SCURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
APPLICATION NUMBER: 08/529,822
FILING DATE: 10-APR-1996
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                                                                                                                                                                TELEX: <UnKnown>
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 42995 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/10125757 Patent No. US20020160410A1 GENERAI INFORMATION:
                 FILING DATE: 10-APR-19 ATTORNEY/AGENI INFORMATION:
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                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
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FRAGMENI TYPE: <Unknown>
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US-10-125-767-17
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Patent No. US20020146785A1
GENERAL INFORMATION:
APPLICANT: Tripathi, G.
APPLICANT: Ramchander, T.V.N.
APPLICANT: Rawal, S.K.
TITLE OF INVENTION: NO.PTA 1579 AND ITS USE TO PRODUCE POLYHYDROXYBUIRATE FILE REFERENCE: A33943 066123.0103
CURRENT APPLICATION NUMBER: US/09/772,364A
CURRENT FILING DAIE: 2001-01-29
NUMBER OF SEQ ID NO.S. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 GAACCTGGACTAGAGAGTCTGCGGCGCGCCCCGAGCCCCAGCGCTTCCCGGCGCGTTAG 174
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49.7%; Pred. No. 1.4;
eative 0; Mismatches 94;
APPLICATION NUMBER: 08/682,080
FILING DATE: 15-JUU-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24631-402J
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-125-767-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.6 SEQ ID NO 1
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TELEX: «UNCOUND
INFORMATION FOR SEQ ID 30: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
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                                                                                                                                                                                                                                                                                                                                                nucleic acid
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US-09-772-304A-1/c
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APPLICANT: Lilie, James
APPLICANT: Drown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: 3bit, Andrew
APPLICANT: Van Huffel, Christophe
APPLICANT: Van Huffel, Christophe
TILLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF HUMAN CANCERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1525 caggaagcccgggggrecrecrecregegrecogggggggggrecsagrrecgaagceceree 1466
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Pred. No, 1.8;
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CURRENT APPLICATION NUMBER: US/39/834,975
CURRENT FILING DATE: 2001-64-13
PRIOR APPLICATION NUMBER: 50/197,538
PRIOR FILING DATE: 2000-04-14
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PRIOR APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOFTWARE: FESLSEQ for Windows Version
SEQ ID NO 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1003, Application US/09834975 Patent No. US20020110815A1
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OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)...(1797)
; OTHER INFORMATION: n = A,T,C or
US-09-834-975-987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 49.03
Matches 95; Conservative
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                                                                                                                                                                                                                            TYPE: DNA CRGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
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Matches 95; Conserv
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LENGTH: 1797
                                                                                                                                                                                          LENGTH: 1797
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                                                                                                                                                                                                                                                                                                   FEATURE:
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APPLICANT: Bolt, Andrew
APPLICANT: Bolt, Andrew
APPLICANT: Van inffel, Christophe
TILLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REPERENCE: MRI-016B
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
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APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20020132090Alel Nucleic Acid and Protein Homologs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 TGGCCGGCTGAACGTCGCCCGTTTAAGGGGCGGGCCCCGGCTCCACGTGCTTTCTGCTGA 343
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                                                                   887 ACCCCAGCGCGACCGGAAGCCGTCCGGCGTCCCCCCCCACACACCACCGCA 828
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Best Local Similarity 51.2%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 103;
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SOF'WARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1386
LENCTH: 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1386, Application US/09833381
Patent No. US20620132090A1
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Paten: No. US20020110815A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
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; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1386
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: POON:
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT APPLICATION DATE: 2001-0117
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 2442
SOFTWARE: PATENTIN Ver. 2.0
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55.4%; Pred. No. 7.3;
ative 0; Mismatches 54;
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Best Local Similarity 49.0%; Pred. Ko. 1.8;
Matches 95; Conservative 0; Mismatches 99;
FILE OF INVENTION: OF HUMAN CANCERS FILE REFERENCE: MRI-016B CURRENT PELLOR NUMBER: US/09/834,975 CURRENT FILING DATE: 2001-04-13 PRIOR APPLICATION NUMBER: 60/197,538 PRIOR FILING DATE: 2000-04-14
                                                                                                                            NUMBER OF SEQ ID NOS: 1046
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1024
LENGTH: 1797
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                                                                                                                                                                                                                                                                                                        LOCATION: (1)...(1797)
OTHER INFORMATION: n = A,T,C or G
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US-09-764-869-2109
                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
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Best Local Similarity
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LENGTR: 15500
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APPLICANT: Lilla, James
APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrew
APPLICANT: Wan Huffel, Christophe
ITLE OF INVENTION: NOYEL GENES, COMPOSITIONS AND METHODS
ITLE OF INVENTION: POR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Van Hiffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION: OF HUMAN CANCERS
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 63/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEG ID NOS: 1046
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1024, Application US/09834975
Patent No. US20020110815A1
                                                                                                                                                                                                                                                                                                      Sequence 1012, Application US/09834975
Patent No. US20020110815A1
GENERAL INFORMATION:
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OTHER INFORMATION: n = A,I,C or G
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US-09-834-975-1624/c
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US-09-834-975-1012/c
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Query Query Score Match Length DB ID	1532 100.0 1643 6 AX060715 AX060894 AX060898 Secure	33.8 93.6 96717 9 AL359182 AL359182 Human	87.b 90.6 183999 6 AXO92589 AXO92589 Sequen 74.4 89.7 2893 6 AX351031	74.4 89.7 3231 6 AX351029 AX351029 Sequen		896 58.5 175064 2 AC012230 AC012230 Homo s	895 58.4 1167 9 HSA252201 AJ252201 Homo s 93.4 58.3 1167 9 AP25862391	08.8 26.7 69570 2 AC021246 AC021246 HOMO	71.8 11.2 69570 2 ACO21246 ACO21246 35.6 8.9 90698 2 ACO21345	28.8 8.4 186889 2 A.807243 AL807243 AL807243 A	28.8 8.4 Z/85/z 10 AF28/263 26.6 8.3 145833 2 AC125837 AC125837	02.2 6.7 2893 6 AX351031 AX351031 9	99.4 6.5 96717 9 AL359182 AL359182	7.8 0.4 49034 9 AF2/5948 AE2/5948 97 6.3 1643 6 AX060715	97 6.3 1643 6 AX060894 AX060894	2 4.5 201144 9 AF287262 AC042589 3	62 4.0 697 9 AF258627 AF258627 E	5.0 3.6 ±91/20 2 ACIO9982 2.6 3.4 125020 9 AF429315	2.2 3.4 125020 9 AF429315 AF429315 F	3.2 96136 2 AC097674 AC097674 1 3.2 173127 2 AC131142 AC131142 B	49 3.2 65780 2 AC111741 F	3.2 13045 2 AC108454 3.2 137136 2 AC108905	8.4 3.2 141114 2 AC108903 AC108903 E	8.4 3.2 205789 2 AC109180 AC109180 N 7.6 3.1 151975 2 AC109403 AC109403 B	7.6 3.1 190543 2 AC097794 AC097794 Rattus	7.4 3.1 101492 2 AC116065 Actius AC116065 Rattus 7.4 3.1 180461 2 AC106563	47 3.1 105983 9 AC108077 AC108077 HOMO SA	3.1 110000 2 ACO96324_0 ACO96324 Rattus	8 3.1 2870 9 HSMB00882 ALT10225 HOMB 8 3.1 169799 2 AC098129 AC098129 Rat	ENTS	AX06071 Sequence	AX060715 AX060715.1 GI:12406104	numan. Homo sapiens	<pre>dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</pre>
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Eomo.
1 (Dases 1 to 1643)
Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
Atp binding cassette transporter protein abcl polypeptides
Patent. WO 007891-A 3 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
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                                             GCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACIGGTGCCCTTGGCTGCCGGGAACGTG
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                /organism="Homo sapiens"
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Direct Submission

Submitted (11-JAN-2002) Wellcome Trust Sanger Institute, Hiaxton, Cambridgeshire, CBIO 15A, W. E-mail enquiries:

cambridgeshire, CBIO 15A, W. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jan 15, 2002 this sequence version replaced gi.1812468.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with this sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempte was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mill subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL: Sw:, SWISSPROT; Tr:, TREMBL: WP:, WORWPEP; Information on the WORWPEP database can be found at
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                 IMPORTANT: This sequence is not the entire insert of clone RP11-21787 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true right end of clone RP11-21787 is at 96717 in this sequence. The true left end of clone RP11-1277 is at 2080 in this sequence. The true right end of clone RP11-122710 is at 72980 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 GATAGAACCACTGATGTGAGTACCTGGGCTTGAG-CGTGGCCTGGAGATCCTGTTGACTG 132
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Heart, Lung and Blood
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3238. 3278
/note="Sequence from AF275948 seque
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Institute, Bethesda, MD 20892, USA.
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http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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Pred. No. 0;
                                                                                                                                                                   /organism="Tomo sapiens/db_xref="taxon:9606"
                                                                                                                                                                                                /chromosome="9"
/clone="RP11-217B7"
                                                                                                                                       location/Qualifiers
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata: Buteleostomi;
Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WC Oll5676-A 1 08-MAR-2001;
University of British Columbia (CA); Xecon Genetics Inc. (CA)
Location/Qualifiers
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97.7%; Pred. No. 0;
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/db_xref="taxon:9606"
37944 c 41170 g 54950
Seguence 1 from Patent WO0115676
AX092589
                        AX092589.1 GI:13444647
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Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P., Brewer, B., Duverger, N., Remaley, A. and Santamarina-Pojo, S. Regulatory nucleic acid sequences of the abol gene Patent: WO 01837(6-A 3 08-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-FEB-2002
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Catarrhini, Hominidae, Homo.
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729 ACAGGGAGGCTGATCAATATAATGAAATTAAAAGGGGGC 'GGTCCCATATTGTTCTGTGT 788
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AX351031
AX351031.1 GI:18616387
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Mammalia; Eutheria; Primates;
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/db_xref="taxon:9606"
681 c 769 q 698
Aventis Pharma S.A. (FR)
Location/Qualifiers
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                      GGGAAICTCCAAGGCAGTAGGTCGCCTATCAAAATCAAAGTCCAGGTTTGTGTGGGGGGAA 2297
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1 (bases 1 to 149034)
Santamarina-Folo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L.,
Cheng,J.F., Osorito,J., Remaley,A., Yang,X.P., Haudenschild,C.,
Prades,C., Chinini,G., Blackmon,E., Francols,T., Duverger,N.,
Rubin,E.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete genomic sequence of the human ABCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7887-7892 (2000)
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Santamarina-Fojo,S., Peterson,K.M., Knapper,C.L., Freeman,L. Remaley,A.T., Yang,X.-F., Haudenschild,C.C., Blackmon,E.E., Francois,T.L. and Brewer,H.B. Jr.
Direct Submission
Submitted (08-JUN-2000) Molecular Disease Branch, National Institutes of Heath, National Heatt, Lung and Blood Institute Bethesda, MD 20892, USA
                                                                                                                                                                                                                                     2598 GCCCGGCGGGGGGAGGGACGCAGGACGCGGAAAGAGACACTGGTGTACCTCCAC
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                                                             2478 CGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGTGG
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AF275948
AF275948.1 GI:9247085
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/db_xref="taxon:9606"
1454. .148034
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DAXKQMKKEIKLAKDSSADRFLNSLGRFWTGLDTRNNVKVWFNNKGWHAISSFLNVIN
NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAXMTTSVDVLVSICVIFAMSFV
                                        FSWFISSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFVFLSVFAVVTLQCFLISTLF
SRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFTLKIFAXLLSPVAFGFGCEFFALFE
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KSYVSSTNLPVLALLLLYGWSITPLMYPASEVPKIPSTAYVVLTSVNLFIGINGSVA
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PEKEVGKVGEWAIRKLGLVKYGEKYAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTG
            PCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIKGIVYBKEARLKETMRIMGLDNSILW
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51246. .61489
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54988
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31050. .31314
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31692. .31973
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36167. .36440
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37617. .37892
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41547. 41565
/gene="ABCAl"
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41657. .41679
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7999. .38166
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38172. .38269
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38995. .39271
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/gene="ABCA1"
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54285. .54418
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41593. .41835
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29916. .30180
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55029. .557
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QQLDGLDWTAQDIVAFLAKEPEDVQSSNGSVYIWREAFNGAIRTISRFMECVNLN
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NKIKDGYWDPGPRADPFEDMRYVWGGPAYLQDVVEQAIIRVLTGTEKKTGVYWQQMPY
110646. 110866,112124. 112196,113183. 113385, 115033. 115010,115297. 115410,116806. 118954, 118604. 118728,119964. 120062,123094. 122283, 124804. 124898,126208. 126240,127363. 127468, 123114. 133114. 133229,133341. 133485,134526. 133116, 135736. 135865,136130. 116250,137088. 137100,138008. 138114,140469. 126250,13708. 131116,142060. 142163,142646. 1425738,143397. 143545, 144581. 1448034)
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/fpt_family="Alu"
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2810. 1900.
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.240. .4509
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Louise, 202 201144 bp DNA linear PRI 29-APR-2001 Homo sapiens ATP-binding cassette l sub-family A member l (ABCAl) and SNAP protein genes, complete cds.
AF287262.1 GI:13876612
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Olu,Y., Caveller,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
Submitted (13-JUL-2000) Genome Science Department, Lawrence
Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,
CA 94720, USA
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1 (bases 1 to 201144)
01u, Y., Caveller, L. Chiu, S., Yang, X., Rubin, E. and Cheng, J.F. Human and mouse ABCAl comparative sequencing and transgenesis studies revealing novel regulatory sequences
Genomics 73 (1), 66-75 (2001)
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အျပည်။	1439631441 /gene="ABCA1"		/number=24 146657. 14685 /gene="ABCA1" /number=25					### Score 1138.2; DB 9; Length 201144; 74.3%; Pred. No. 76-294; 7-6-294; 7-6-38 54; Gaps 1	16 GCTCCACATGCACTCCAGGCCTGCTTGGCTCTTCTATGGGTCTGTCCTGAGGTT 73 1	GATAGAACCACTGATGTGAGTACCTGGGGTTGAG-CGTGGCCTGGAGATCCTGTTGACTG 132	TAGCATGGAGGGGGTIGT-CACCTGAATGTCTGTATGCAGGTGGTGGAGTTCTGGAAI 191 	AIGATGGAGCTGGAGGTGGGAAGAGAAGTAGGCTTGGGGGAGCTCTCTCATGCCACCTCA 251	TTCTGGCCAAACTCAGGTCAACTGTGAAGGTCTAAATGTGAATCTGCCCTTCAAGGT 311 	GGCTACAAAGGIATCTTGTCAAGGTAGGAGACCTTGTGGGCCTCCAGGAGTTCCAGGATTLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	372 GCCTGCTT-GGCCICTTCTACGGGTCTGCTGAGTCTTCTATGAATCT-CCCTTCAGGG 429 [11] [1] [1] [1] [1] [1] [1] [1] [1] [1	CAGATICATATITAGACICTICACAGITIGACCIGAGITITGGCCAGAATAAGGIGACAT 489	490 TIAGTTIGTTGGCTTGATGAATGACTTAAATATTTAGACATATGGTGTGTAGGCCTGCAT 549	TITTGCCCCTCCAGTGTTIGGGTAGTTTTGCTCCCCCTACA 609	GCCAAAGGCAAACAGATAAGTTGGAGGTCTGGAGTGGCTACATAATTTTACACGACTGCA 86

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4 bp DNA linear HTG 22-APR-2000
0, WORKING DRAFT SEQUENCE, 39 unordered
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                    GCCCCTTAAAAGAACTAGGTACCTTAAGCT 33274
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REFERENCE AUTHORS REFERENCE

TITLE

COMMENT

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17 48215: gap of 100 bp 17 52618: contig of 4402 bp in length 19 52718: contig of 4402 bp in length 19 55592: contig of 3874 bp in length 19 56692: gap of 100 bp 593 55635: contig of 2943 bp in length 16 5735; gap of 100 bp 100 bp 63661: contig of 3926 bp in length
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f 6678 bp in length
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101: gap of 100 bp
103016: contig of 5015 bp in length
103016: gap of 100 bp
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145492 145591; gap of 100 bp
145592 157391; contig of 11800 bp in length
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contig of 4676 bp in length
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                                                                                                                                                                                   34299; contig of 2861 bp in length 199; gap of 100 bp 2818; contig of 3919 bp in length 118; gap of 100 bp 42835; contig of 4417 bp in length
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84: gap of 100 bp
31338: contry of 3054 bp
                                       p of 100 bp contig of 2356 bp
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/note="assembly_fragment"
4516. .5785
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/db_xref="taxon:9506"
22587: contig of 26
22587: cr
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28184: contig of
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68437; cont.
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124079: conti
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                                                                                               Submitted (21-CCI-1999) Whitehead Institute/MIT Center for Genome secarch, 320 Charles Street, Cambridge, MA 02141, USA Apr 22, 2000 this sequence version replaced gi:6454033. All repeats were identified using RepeatMasker:
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@enome.wi.mit.edu
Contact: requence_submissions@enome.wi.mit.edu
Contact project Information
Conter project Information
Conter project name: L2510
Center close name: L3510
Center close name: L3510
Center close name: L3510
Consensus program: Phrap: wrsion 0.960731
Consensus quality: 117571 bases at least Q40
Consensus quality: 145749 bases at least Q30
Consensus quality: 166940 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 171264; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; sum-of-contigs
Quality coverage: 3.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                       Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; (bases i to 175054)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo, Sapiens, clone RF1:-1M10
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1004 1103: gap of 100 bp
1104 2634: contig of 1531 bp in length
2635 273; gap of 100 bp
2735 4415: contig of 1681 bp in length
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f 1994 bp in length
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Web site: http://www-seq.wi.mit.edu
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Porsch-Czcurumez,M., Langmann,T., Heimerl,S., Borsukova,H., Raminski,W.E., Drobnik,W., Honer,C., Schumacher,C. and Schmitz,G. The zinc finger protein 202 (ZNF202) is a transcriptional repressor of ATP binding cassette transporter AI (ABCAI) and ABCGI gene expression and a modulator of cellular lipid efflux 2.1 Biol. Chem. 276 (15), 12427-12433 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRI 10-APR-2001
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1 (bases 1 to 1167)
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Porsch-Oezcueruemez,M.K.
Direct Submission
Submitted (05-5N-2000) Porsch-Oezcueruemez M.K., Institute for Clinical Chemistry, Universitiy of Regensburg, FRanz-Josef-Strauss-Allee 11, 93042 Regensburg, CERMANY Location/Qualifiers
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                                                                                          1165 CAAATICCACTGGTGCCCTTGGCTGCCGGAACGTGGACTAGAGAGTCTGCGGCGCAGCC
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/mote="assembly_fragment"
68538. .71458
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/note="assembly_fragment"
34400. .38318
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38419, .42835
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48217. .52618
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52719. .56592
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/note="assembly_fragment"
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10232. .22587
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22688. .25707
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25808, .28184
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28285. .31338
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31439. .34299
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17301. .20131
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9787. .12253
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/db_xref="taxon:9606"
/chromosome="9"
/map="9631"
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                                                                    /function="cholesterol efflux regulatory protein" 896. .900
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                          /map="9922-31"
/cell_type="leukocyte"
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/gene="ABC-1"
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larity 99.9%;
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CE 1 (bases 1 to 1167)

RS Pullingar.C.R. Hakamata.H., Duchateau.P.N., Eng.C.,
Analysis of habcl gene 5' end: additional peptide sequence,
promoter region; and four polymorphisms

AL Bloccem. Siophys. Res. Commun. 271 (2000) In press

CE 2 (bases 224 to 1167)

RS Pullingar.C.R. Hakamata.H., Duchateau.P.N., Eng.C.,
Anuzerat.B.E., Fleiding.C.J. and Kane,J.P.

Submitted (20-APR-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San
Francisco, CA 94143-0130, USA

S Pullinger.C.R. Hakamata.H., Duchateau.P.N., Eng.C.,
AL Submission

AL Submitted (23-JUN-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San
S Pullinger.C.R. Hakamata.H., Duchateau.P.N., Eng.C.,
Autisant.B.E., Fielding.C.J. and Kane,J.P.
Direct Submission

AL Submitted (23-JUN-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue,
Submitted (23-JUN-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue,
S sequence update by submitter
On Jun 23, 2000 this sequence version replaced gi:7769713.

Location/Qualifiers

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Homo sapiens ATP binding cassette transporter 1 (ABCA1) gene,
promoter and even 1
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E (bases 1 to 59570)

Biren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldakin, J., Barna, N., Beckerly, R., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cocke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferrelra, P. Fitzhugh, W., Forrest, C., Gaqe, D., Galagan, J., Rerrelra, P. Fitzhugh, W., Forrest, C., Gaqe, D., Galagan, J., Randas, S., Grant, G., Egos, B., Heaford, A., Horton, L., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marqiis, N., McEwan, P., McGurk, A., McKernan, K., Macdonald, P., Marqiis, N., McEwan, P., Olivar, T. M., Peterson, R., Pisrer, C., Forner, C., Pisrer, C., Connor, T., O'Donnell, P., Olivar, T. M., Peterson, R., Pisrer, C., Santos, R., Santos, R., Severy, P., Spencer, B., Stange-Thoman, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 13, 2000 this sequence version replaced 91:6705871.

All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This record contains 73 individual
* sequencing reads that have not been assembled into
* cortigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smir, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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10376: contig of 846 bp in length
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11322: contig of 846 bp in le
12302: contig of 880 bp in le
2402: gap of 100 bp
13280: contig of 878 bp in le
3380: gap of 100 bp
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Web site: http://www-seq.wi.mit.edu
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1/9: gap of 9430: cc.
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11423 12302: conti
12303 12402: gap of
12403 13280: conti
13281 13380: gap of
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 59570)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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Unpublished
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Homo sapiens
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if 348 bp in length
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45744: contig of 872 bp in length
24: gap of 100 bp
46643: contig of 819 bp in length
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2483; gap of 100 bp
25570: contig of 837 bp in length
2570; gap of 100 bp
26621: contig of 851 bp in length
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19009: contig of 868 bp in length
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15196: contig of 855 bp in
96: gap of 100 bp
16123: contig of 827 bp in
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38083: contig of
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ilarity 99.1%; Pred. No. 3.5e-98;
Conservative 0; Mismatches 2;
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58130: contig of 867 bp ir

1 58230: gap of 100 bp

59082: contig of 852 bp ir

3 59182: gap of 100 bp

60020: contig of 838 bp ir
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f 852 bp
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53328: contig of 856 bp
53428: gap of 100 bp
54258: contig of 840 bp
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ACCESSION VERSION KEYWORDS

SOURCE

REFERENCE

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18041: contig of 869 bp in length
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contig of 857 bp in length
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20921: contig of 855 bp in length
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10376: contig of 846 bp in length
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[5196: contig of 855 bp in
96: gap of 100 bp
6123: contig of 827 bp in
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59 35204; contig of 836 bp in

53 35304; gap of 100 bp

57 36256; gap of 100 bp

57 36256; gap of 100 bp

59 37228; gap of 100 bp

29 38283; contig of 872 bp in

29 38283; contig of 855 bp in

34 38183; gap of 100 bp
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f 870 bp in
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100 pp
16721: gap of 100 hr
16726: conti
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contig of 853 bp in
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21865: contig of 844 bp
21965: gap of 100 bp
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30455: contig of 863 bp
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contig of 855 bp
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contig of 858 bp
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F 861 bp
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23780: contig of 848 bp
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11322: contig of 846 bp
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14241: centig of 8
341: gap of 10
15196: contig of 8
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33312: com
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2 (Dases I to 69570)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Ailen, N.,

Birren, B., Linton, L., Barna, N., Beckeriy, R., Beda, F.

Anderson, S., Baldwin, J., Barna, N., Beckeriy, R., Beda, F.

Boguslavkiy, L., Boukhqaiter, B., Brown, A., Burkett, G., Castle, A.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,

DeArellano, K., Dowar, K., Domino, M., Doyle, M., Fenestor, J.,

Ferreira, P., FitzHugh, M., Forrest, C. Gago, J., Galagan, J.,

Gardyna, S., Grant, G., Hagos, B., Beaford, A., Borton, L.,

Howland, J.C., Johnson, R., Jewich, M., Maratas, A., Klein, J.,

Landers, P., Lahorozky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,

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McDheeters, R., Meldrim, J., Mereus, L., Norrow, J., Naylor, J.,

Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, R.,

Stojanovic, N., Savery, P., Spencer, B., Stange-Thomann, N.,

Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,

Direct Submission, M., Mitchhand, Tartithe, Arm Conter for Content of Cont
                                                                                                                                                   HTG 13-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-7AN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence Version replaced gi:6705871. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                    ACU21246 69570 bp DNA linear HTG 1
Homo sapiens clone RP11-1N10, LOW-PASS SEQUENCE SAMPLING.
AC021246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              will be sequenced to completion. In the event that the record is updated, the accession number will
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                                                                                                                                                                                                                                                                                                                                                    Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome, clone RP11-1N10
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Web site: http://www-seg.wi.mit.edu
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972 1834: cc
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                                                                                                                                                                                                                                                                                                                  Mammalia, Eutheria, P)
1 (bases 1 to 69570)
                                   41529 GATCTATAAAAGGAA 41544
              1517 GAATCTATAAAAGGAA 1532
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                                                                                                                 RESULT 13
AC021246/c
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JOURNAL
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TITLE
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AUTHORS
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COMMENT

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100 bp
of 840 bp in length
103 bp
of 861 bp in length
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856 bp in length
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f 834 bp in length
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contig of 864 bp in length
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                                                                                        24: gap of 100 bp
43776: contig of 852 bp in length
      40006: contig of 975 bp 40106: gap of
                            06: gap of 100 bp
40967: contig of 861 bp
067: gap of 100 bp
41913: contig of 846 bp
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50440: contig of 855
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48551: contig of 852
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58130: 7
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47599: cont
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49485: cont.
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60983: cont
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60023: cont
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59082: con
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53328: con
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42825
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Query Match 11.2%; Score 171.8; DB 2; Length 69570; Best Local Similarity 87.7%; Pred. No. 1.4e-34; Matches 185; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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Dipublished

Sirren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barran, N., Beckerly, R., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Bodslay, L., Bowar, K., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, K., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dowar, K., Domino, M., Doyle, M., Ferestor, J., Galagac, J., Gardyna, S., Grart, G., Hagos, B., Heaford, A., Horton, L., FitzHugh, M., Forrest, C., Gage, J., Gardagac, J., Landers, T., Lehoczky, J., Leine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Morwan, P., Mcdurk, A., McKernan, K., Marquis, N., Merwan, P., Mcdurk, A., McKernan, K., Norman, C. H., O'Connor, T., C'Donnel, P., Olivar, T. M., Peterson, K., Pisaci, C., Poliara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Sartos, R., Severy, P., Speneer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wu, X., Wyman, D., Ye, W. Jimmer, A. and Zody, M., Yel, R., Vo, A., Wu, X., Wyman, D., Ye, W. Jimmer, A. and Zody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, N., Jimmer, A. and Zody, M., Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, M. Ollyl, USA On Jul 13, 2000 this sequence version replaced gi:6705761.

All repeats were identified using RepeathWasker hand
                                                                                                                                                                                                                                                                                                                                                                  AC021345 13-JUL-2000 DNA linear HTG 13-JUL-2000 HOMO sapiens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING. AC021345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research
1442 AGAGGCCGGGAACGGGGGGGGGGGGGGGGGGCGCTTTGACCGATAGTAACTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-24J9
Unpublished
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Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                  Information
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Center clone name:
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HIG: HTGS_PHASE0.
Homo sapiens.
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(bases 1 to 90698)
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AC021345/c
LOCUS
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46305: contig of 880 bp in length
105: gap of 100 bp
47302: contig of 897 bp in length
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Pred, No. 7.5e-25;
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                                    81 40407; contig of 927 bp in 38 40507; gap of 100 bp in 98 41405; contig of 898 bp in 641505; gap of 100 br
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57225 58121: contig of 897 bp
58122 58221: gap of 100 bp
58122 59075: contig of 834 bp
5976 59175: gap of 100 bp
59176 60058: contig of 883 bp
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65015: contig of 889 bp
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870 bp
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51209: contig of 859 bp
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57124: contig of 859
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...: contig of 8:
7175: gap of
60658: ~.
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4: gap of
64026: ~
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68934: 7
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14: gap of
69910: ما
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J: gap of

40407: c

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Best Local Similarity 55.1%:
Matches 172: Conservative
  22: gap
38402: c
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f 866 bp in length
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15434 36440: contig of 907 bp in length
16441 36540: gap of 100 bp
16541 37422: contig of 882 bp in length
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20734: gap of 100 bp in length
20734: gap of 100 bp in length
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contig of 899 bp in length
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f 859 bp in length
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886 bp in length
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37: gap of 100 bp
27464: contig of 877 bp in length
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898 bp in length
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17678: contig of 901 bp in length
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of 908 bp in length
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if 843 by in length
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883 bp in length
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                               10 bp

16 378 bp in

100 bp

6 914 bp in led

bp in
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547: gap of 100 hr
34435: conft
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5 901 bp in
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of 905 bp in
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f 902 bp
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of 904 bp i
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14684: contig of 874 bp
84: gap of 100 bp
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16677: contig of 915 bp
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                 of 100 bp
contig of 851 bp
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24554: contig of 886
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25521: contig of 867
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15662: contig of
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18679: cc
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11732: cont
11832: gap of
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23568: con
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5759: conf
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8755: con
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9753: con
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6764: con
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4816: cor
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95 60756; contig of 2402 bp in length

87 60886; gap of 100 bp in length

87 66707; contig of 821 bp in length

86 6807; gap of 100 bp

86 92102; contig of 25295 bp in length

83 92202; gap of 100 bp
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1: contig of 4271 bp in length
gap of 100 bp
8: contig of 5047 bp in length
gap of 100 bp
4: contig of 2526 bp in length
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contig of 30472 bp in length.
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163: qzp of 100 bp 40087: contig of 10024 bp in length 4887: qap of 100 bp 44438: contig of 4251 bp in length
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f 7707 bp in length
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6905 bp in length
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contig of 9143 bp in length
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                                                                 38: gap of 100 bp 48960: contig of 4422 bp in length 60: gap of 100 bp 56007: contig of 6947 bp in length
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11174 bp in
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fragment_chain:1"
55108. 58284
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/note="assembly_fragment:01920
fragment_chain:1"
4950. .2267
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/note="assembly_fragment:00140
fragment_chain:1"
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/note="assembly_fragment:00335
fragment_chain:1"
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/note="assembly_fragment:01430
fragment_chain:1"
49061. .56007
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/cote="assembly_fragment:00965
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fragment_chain:1"
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fragment_chain:1"
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/chromosome="4"
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9: contig of
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156318 156417; gap of
156418 186889; conti
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144549 147074: con+1
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139301: conti
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58284: con+
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                                                                                                                                                                                                                                                                                                                                                                                                                              ALB07243 linear HTG 3C-CJN-2002 Mus musculus chromosome 4 clone RP23-25D17, *** SEQUENCING IN PROGRESS ***, 24 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (29-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: hunguery@sanger.ac.uk Cloone requests: clonerequest@sanger.ac.uk on Jul 2, 2002 this sequence version replaced gi:21668136.
                                                                                                                                                                                                                                                         87685
                                                                                                                                                                                                                                          1461 GGGAGGAGGAGCACAGGCTTGACCGATAGTAACTCCGCGCTGCGTGCAGCGAAT 1520
     Quality coverage: 4.72x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                            1401 GCCTCCACGTGCTTTCTGCTGAGTGACTACATAAACAGAGGCCGGGAACGGGGCG
                                                                        100 bp
of 17671 bp in length
100 op
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Chemistry: Dye-terminator; 100% of reads
Consensus quality: 175599 bases at least 040
Consensus quality: 179463 bases at least 040
Consensus quality: 179463 bases at least 030
Consensus quality: 180169 bases at least 030
Insert size: 184569; sum-of-contigs
Insert size: 184569; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coverage: 4.82x in 020 bases; agarcse-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jenter: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: numquery@sanger.ac.uk
------ Project Information
Center project name: bM25D17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4850 4949: gap of 10
4950 22620: contig of
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ALIGNMENTS

Human large AIP-binding cassette transporter 1(hABCl) promoter sequence. Human; large ATP-binding cassette transporter 1; ABC1; promoter; antiarteriosclerotic; gene transfer; transactivator; ds. BP. ABL58400 standard; DNA; 1197 (first entry) 30-JUL-2002 ABL58400; RESULT 1 ABL58400

WO200183506-A Homo sapiens 08-NOV-2001.

28-APR-2000; 2000US-0560372. 27-APR-2001; 2001WC-US13654

Tall AR;

(UYCO) UNIV COLUMBIA NEW YORK

XX PA XX

WPI; 2002-049334/06.

Novel isolated human large ATP-binding cassette transporter 1 promoter capable of directing transcription of heterologous coding sequence positioned downstream to it, useful for expressing foreign DNA in host

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The invention relates to an isolated human large ATP-binding cassette transporter 1 (ABC1) promoter capable of directing transcription of betachogous coding sequence positioned downstream to it. The ABC1 promoter is useful for expressing foreign DNA in a host cell, by introducing into the host cell a gene transfer vector comprising the introducing into the host cell a gene transfer vector comprising the promoter operably linked to a foreign DNA encoding a desired polypeptide or RNA, where the foreign DNA is expressed. The gene transfer can be introduced into the host cell by adenovirus infection, liposome-mediated transfer condes and expresses a reporter molecule. The method transfer vector encodes and expresses a reporter molecule. The method further involves introducing into the cell a gene transfer vector comprising a cucleic acid segment encoding a transactivator protein capable of upregulating the ABC1 promoter, or contacting the cell with
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                                                                                                                                                                                                                                                                                                         Claim 1; Fig 3; 68pp; English.
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0 100.0%; Score 463; DB 24; Length 1197; 100.0%; Pred. No. 7.8e-108; Indels Mismatches 0; Conservative Query Match Best Local Similarity Matches 453;

1078 1018 1079 GGCARARACCCGTAATTGCGAGCGAGCGAGTGGGGCCGGGACCCGCAGGCCGAGCC 1138 360 180 420 1 CCTIGGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGCGCAGCCCGAGCCCAGCGCTTC 60 CCGCGCGTCTTAGGCCGGCGGGGCGGGGGGGAAGGGGAACGCAAAGGGGAACCTAAA GACACCTGOTGTACCCTCCACCCCACCCCACCCACCTCCCCCAACTCCCTAGATGTGT GACACCTECTGTACCCTCCACCCCCACCACCTCCCCCCCCAACTCCTAGATGTGT CGTGGGCGGCTGAACGTCGCCCGGTTTAAGGGGCGGGCCCCGGCTCCACGTGCTTTCTGCT CTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCGAATCTATAAAAGGAACTAGTCCC CTTTGACCGATAGTAACCTCTGCGCTCGGTCCAGCCSAATCTATAAAAGGAACTAGTCCC 719 779 839 899 626 1019 59 121 181 241 301 qq q õ Q ð õ q ΩY 97 δ õ ã

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AAF24681 standard; DNA; 1643 BP. AAF24681: AAF2468. XX AC XX DT XX DT

RESULT 2

(first entry) 20-APR-2001 Nucleotide sequence of the 5' flanking region of the human ABCl gene.

Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier Gisease; chromosome 9q22-9q31; heart disease; hypercholesterolemia;

CITTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAATCTATAAAAGGAACTAGTCCC

301

Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosolerosis. cholesterol transport; 99US-0153872. Garvin M; 2000WO-US16765 99US-0140264 (CVTH-) CV THERAPEUTICS INC WPI; 2001-137812/14. Lawn RM, Wade D, atherosclerosis; MO200078972-A2 Homo sapiens. 16-JUN-2000; 14-SEP-1999; 19-NOV-1999; 18-JUN-1999; 28-DEC-2000

The present sequence represents the 5' flanking region of the huuman adenosine triphosphate (AIP) binding cassette protein (ABC) 1 gene. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipcprotein-mediated mobilisation of intracellular colosterol stores. ABC1 is defective in Tangier disease, a genetic disease, a constitution of intracellular diseaser about a protein and society of abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9d22-9g31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of and atheroscierosis. The genes associated with hypercholesteroleming assays and atheroscierosis the genes are useful for developing screening assays the screen of the correct to screen for compounds that regulate the expression of genes associate with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.

Claim 1; Page 143-144; 215pp; English.

0

Sequence 1643 BP; 370 A; 413 C; 457 G; 403 T; 0 other;

ó 1181 CTTGGCTGCCGGGAACGTGACTAGASAGTCTGCGGCCCAGCCCCGAGCCCAGCGCTTC 1240 Gaps 09 1 CCTTGGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGCGCAGCCCCGAGCCCAGCGCTTC 1361 CGTGGGGGGTGAACGTCGCCGGTTTAAGGGGGGGGGGGCCCCGGCTCCACGTGCTTTCTGCT CCGCGCGCTTTAGGCCGGCGGGGGGGGGGAAGGGGACGCAGACCGCGGGACCTAA GACACCTECTGTACCCTCCACCCCCACCCCACCTCCCCCCAACTCCCTAGATGTGT CGIGGGGGGCIGAACGICGCCGITTAAGGGGGGGGCCCCGGGCICCACGIGCTTTCIGCT 0; Length 1643; Indels 100.0%; Score 463; DB 22; 100.0%; Pred. No. 8.2e-108; ive 0; Mismatches 0; Best Local Similarity 100. Matches 453; Conservative Query Match 121 1301 181 241 61 1421

QC δž

δŽ QQ δ qq ${\bf Q} {\bf y}$ q QΫ́ g ΩY Db

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The present sequence represents the 5' finaking region of the huuman adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABCI resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABCI is a pivoral protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABCI is defective in Tangler disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABCI gene is localised to chromosome 9q22-9q31. The ABCI genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful for are also useful for an elso useful as diagnostic indicators of cardiovascular disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adenosine triphosphate (ATP) binding cassette protein (ABC) l
polynucleotides and polypeptides, useful for treatment of heart disease
and other disorders associated with hypercholesterolemia and
of the human ABC1 gene.
                                                                                                                                                                                                                                                                                                                              Human; adenosine triphosphate binding cassette protein 1; ABC1; poblipoprorein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1643 BP; 370 A; 413 C; 457 G; 403 T; 0 other;
                                                                                     also useful as diagnostic indicators of cardiovas
er disorders associated with hypercholesterolemia.
                                                                    sequence of the 5' flanking region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garvin
                                                                                                                                                                                            ВP
                                                                                                                                                                                          AAF24703 standard; DNA; 1643
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99US-0153872.
99US-0166573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000WO-CS16591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CVTH-) CV THERAPEUTICS INC. (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oram JE,
                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-137811/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wade D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atherosclerosis
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14-SEP-1999;
19-NOV-1999;
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                                                                                                                                                                                                                                                                                               Nucleotide
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Treating a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity -
            1240
                                                                                                                                                                                         1480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
CGTGGGCGGCTGAACGTCGCCCGTTTAAGGGGCGCCCCGGCTCCACGTGCTTTTTGTCT
                                                                                                                                             1361 GETGGGGGGGGAACGTCGCCGGTTTAAGGGGGGGGGCCCCGGCTCCACGTGCTTTCTGCT
                                                                                                                                                                                                              CTITIGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAATCTATAAAAGGAACTAGTCCC
                                                                                                                                                                                                                          CCGCGCGTCTTAGGCCGGCGGGCCGGGGGAAGGGGACGCAAACCGCGGAACCTAA
                                                                           GACACCTGCTGTACCCTCCACCCCCACCCCACCCACCTCCCCCCAACTCCCTAGATGTGT
                                                                                                                                                                                                                                                         The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal
                                                                                                                                                                                                                                                                                                                SM;
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                                                                                                                                                                                                                                                                                                      GACCCTTCTCTCCCGGCTGCGGCAGGCCAGGGCGGGGAGCTC
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23-JUN-2000; 2000US-0213958.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ABC1 genomic DNA
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Length 1643; Indels

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100.0%; Score 463; 100.0%; Pred. No. 8

1 CCTTGGCIGCCGGSAACGTGGACTAGAGACTCTGCGGCGCAGCCCCGAGCCCASCGCTTC 60

Mismatches

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Conservative

Similarity

Query Match Best Local Simi. Matches 463; (

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The invention relates a nucleic acid which is capable of regulating the transcription of human ATT-binding cassette 1 (ABC1) gene, which is a casual gene for pathologies linked to a dysfunctioning of cholesterol metabolism, including diseases such as atherosclerosis. Polynucleotides of the invention are used to screen candidate molecules or substances that are capable of modulating the transcription of the ABC1 gene. They are used in antisense therapy. Compositions comprising sequences of the invention are used to treat hypercholesteroleamia and atherosclerosis. The present sequence is human ABC1 transcription regulating DNA.
                                                               Isolated nucleic acid useful for modifying the ATP-binding cassette {\bf 1} (ABC1) and screening for candidate modulatory compounds or substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGCGCGCTCTTAGGCCGGGCGCGCGGGGGGAAGGGGGACGCAGACGGGGACCCCTAA 120
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   Santamarina-Fojo
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Pred. No. 1.5e
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                                                                                                                              Claim 1; Page 130-131; 152pp; English.
   Remaley A,
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Best Local Similarity 96.7%;
Matches 462; Conservative
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   Duverger
                                 WPI; 2002-154404/20
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   Brewer
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                                                                                                                                                            Length 183999;
triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR or EXR*mediated transcriptional activity or ABC1 expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition lower than normal EDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
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                                                                                                                                                       96.5%; Score 447; DB 22;
ilarity 98.7%; Pred. No. 2.1e-103;
Conservative 0; Mismatches 1;
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                                                                                                                                                                         Similarity
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Matches 462;
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iers	"LMO2COM/MYCD"	"DeltaEF1"	"S8/NKX2.5"	"S6"	"GATA"	" <u>TK2"</u>	"LYP1"	"JMO2COM/MYOD/DeltaBFl"	"LYF1"	"DeltaBF1"	"LXX2.5"	"NFY/CAAT"	"TEZM"	"TāZM"	"HFH2/SRY/EVIl"	"CREBP1_VBP"	"NKX2.5"	"GATA"	"LXRalpha/de:taEF1"	"DeltaEF1/LYF1/IK2"	"Ap4"	"LMO2-COM/WYOD/deltaEP1/E47"	"ZID/deltaEF1"
Socation/Qualifiers	a moiety=	F.	=	d oiety= "	ety=	f oiety=	g oiety≕	h oiety= "IMO2COK/MYOD/D	/*tag= i /bound_moiety= "LYF1" 558 568	/*tag= j /bound_moiety= "DeltaBF1" 59059	"LXX2.	l oiety=	m noiety= "MZFl)	n _moiety= 85	"HFH2/SRY/EVI1	/*tag= p /bound_moiety= "CREBP1/VBP" 831837	r olety= "NKX2 89	"GATA	ty= "LXRalpha/deltaEF1	"DeltaEF1/LYF1/	ety=	ty= "LMO2-COM/MYOD/	/=====================================

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2877 GTCCCGGCAAAACCCCGTAATTGCGAGCGAGAG 2910
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Matches 120; Conserv
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                                                                                                                                                                                                                                                                                                         "IMOSCOM/MYOD/E47"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "USF/NMYC/ARNT"
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2794..2806
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2634..2648
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                                                                                                                                                                                                                                            expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403 GACCCGCAGAGCCGACCCTTCTCCCGGGCTGCGGCAGGGCAGGGCGGGGAGCT 462
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                                                                                                                                                                               Human secreted protein 5' EST, SEQ ID NO: 13690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID 13690; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                             gene therapy; chromosome mapping; ss
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AAC09615 standard; cDNA: 227 BP
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99.2%;
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replace(2969,G)
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AAI70315,
                                                                                                                                                                                                              Key
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0;
                                                                                                                                  Human: AIP binding cassette transporter 1; ABC1; coronary heart disease; dermatological; atheroscierosis; cardiovascular; inflammatory disease; psoriasis; lipid disorder; antibacterial; septic shock; gene therapy; immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to four common polymcrphisms in the gene encoding dargesette transporter-I (ABCI). ABCI is associated with decreased ApoA-I mediated efflux of cholesterol. The polymcrphisms in ABCI directly affects cellular lipid homeostasis, which is a key factor in the atherogenetic processes. The ABCI polymcrphisms are useful for diagnosing and treating lipid disorders, cardiovascular diseases (coronary heart disease, atherosclerosis) and inflammatory diseases transporter for interleckin-ibeta (IL-lbeta) identification of ABCI as a candidate for treatment of inflammatory diseases including rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366 AAACCCCGTAATTGCGAGCGAGCGAGTGAGTGGGGCCGGGACCCGCAGCCGAGCCGACCC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AAACCCCGTAATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGACCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arthritis and septic shock. The present sequence is human ABC1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New adenosine triphosphate binding cassette transporter-1 gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.2%; Score 98; DB 22; Length 7260; 100.0%; Pred. No. 2.5e-15; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7260 32; 1834 A; 1765 C; 1905 G; 1756 I; 0 other;
                                                                                                        Human ATP binding cassette transporter 1 (ABC1) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TICTCTCCCGGGCTGCGCCAGGGCAGGCCGGGGAGCTC 463
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                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 1; 48pp; English.
              AAD21326 standard; DNA; 7260 BP.
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les 98; Conserv
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EP1136552-A1

25-SEP-2001

Schmitz G,

Homo sapiens

28-JAN-2002

AAD21326;

AAD21326

AAI70315 standard; cDNA; 7260 BP.

RESULT 9 AAI70315

Query Match

Matches

426 ...9

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The present sequence is that of cDNA encoding the human adenosine triphosphate (ATP) binding cassette transporter 1 (ABC1) protein (see AAM50227). The sequence includes an extended open reading frame (ORF) to that provided by the sequence in AAT70314, using an alternative ATG codon as initiation codon and thereby adding an extra 40 N-terminal amino acids to the encoded ABC1 protein (see AAM50228). The invention provides 4 common polymorphisms in the ABC1 gene. These were identified by sequencing the ABC1 gene in different Tangier kindreds. In the variant genes (unmbering as in AAT70314), G is changed to A at position 596, T is changed to C at position 1356, A is changed to G at position 1356, or any combination of these. All of these collymorphisms alter the amino acid sequence of ABC1 and therefore may affect its function. The 2 most common polymorphisms (G596A) and A2589G) are both associated with a decreased in vitro ApoA-1 mediated efflux of cholesterol from monocuclear phagocytes, a catalished coronary heart disease. 3 of the variants (G596A, A2589G and G3456C) are significantly increased in a population of mediated efflux of the angels (G596A) are significantly increased in a population of established coronary heart disease. (ED) relative to CHD-free control subjects. The use of the provided ABC1 polymorphisms for the diagnosis and treatment of lipid disorders, cardiovascular current and infimammatory diseases (e.g. psoriasis, lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= b
/note= "alternative open reading frame of AAI70314"
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                                                                                                  ATP binding cassette transporter 1; ABC1; human; lipid disorder; cholesterol; cardiovascular disease; inflammatory disease; antiinflammatory; antilipease; artipsoriatic; dermatological; angier disease; coronary heart disease; diagnosts; gene therapy;
Human ATP binding cassette transporter 1 (ABC1) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 25-28; 41pp; English.
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321..7106
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qq ζĊ 90

9995×8

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AAH07432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y. Compositions comprising sequences of the hypercholesterolaemia and atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid useful for modifying the ATP-binding cassette 1 (ABC1) and screening for candidate modulatory compounds or substances \,
                                                                                                                                                                                                                                                                  366 AAACCCCGTAATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGAGCCGACCC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ATP-binding cassette 1; ABC1 gene regulation; atherosclerosis;
                                                                                                                                                                                                                Gaps
                           also
                                                                                                                                                                                                                                                                                              cholesterol metabolism; hypercholesterolaemia; antisense therapy
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                                                                                                                                                                                                                0
erythematodes) is claimed. Modulation of ABC1 transcripts or proteins by antisense or ribozyme technology or {\tt RNA} decoys is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Denefle:
                                                                                                                                                           Score 98; DB 22; Length 7260; Pred. No. 2.5e-15;
                                                                                                      Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s C, Lemoine C, Naudin L, D
Remaley A, Santamarina-Fojo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.7%; Score 91; DB 24; L
100.0%; Pred. No. 8.2e-14;
. Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 221 BP; 44 A; 62 C; 73 G; 42 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is human ABC1 gene exon 1A.
                                                                                                                                                                                                                                                                                                                                                                            426 TICICICCGGGCTGCGCCAGGCCAGGCCGGGGAGCTC 463
                                                                                                                                                                                                                                                                                                                                                                                                             61 TTCTCTCCGGGCTGCGGCAGGCAGGGCGGGGGGGGCTC 98
                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 132; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are used in antisense therapy. invention are used to treat hyp
                                                                                                                                                              21.2%; 8
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-2001; 2001WO-EP05488.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD37268 standard; DNA; 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ous M, Prades
Duverger N, F
                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ABC1 gene exon 1A.
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                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200183746-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-2001
                                                                                                                                                                                                                   98;
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                                                               claimed
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0;

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Indels

Length 221;

373 STAATIGCGAGCGAGAGIGAGIGGGGCCGGGACCCGCAGAGCCGAGCCGACCCITCIC 432

100.0%; Pred. ...

91; Conservative

Matches

δà

Local Similarity

Query Match

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The present invention describes primer sets for synthesising 5602

(11.1ength cDNAs defined in the specification. Where a primer set

(21.1ength cDNAs defined in the specification. Where a primer set

(22. comprises: (a) an oligon-dry primer and an oligonuclectide comprises one of

(23. comprises at least 15 incleotides promprises one of

(24. comprises at least 15 incleotides; or (b) a combination

(25. comprises at least 15 incleotides; or (b) a combination

(26. da oligonucleotide comprises at least 15 incleotides; or (b) a combination

(27. complementary strand of a polynucleotide which comprises a 5'-end

(28. sequence and an oligonucleotide comprising a sequence complementary to the

(29. complementary strand of a polynucleotide which comprises a 3'-end sequence, where the complementary to

(20. principation and primer sets and lossed in antisense therapy and

(37. end sequence/3'-end sequence is selected from those defined in

(38. comprises at least 15 nucleotides and the combination of

(49. comprises at least 15 nucleotides and the combination of

(50. complementary). The primers are useful for synthesising polynucleotides,

(50. particularly full-length cDNAs. The primers are also useful for the

(50. detection and/or diagonosis of the abnormality of the proteins encoded by

(50. connas easily without any specialised methods AAB03166 to AAB13628 and

(50. AAB95893 represent human amino acid sequences; and AAB13629 to AAB13632

(50. content oligonucleotides, all of which are used in the exemplification

(50. content invention.
                                                                                                                                                                                                                                                                                                                                          primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saito K,
Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 736 BP; 163 A; 199 C; 199 G; 170 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 4267; 2537pp - CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                      SEQ ID NO:4267.
                                                            463
                                                                                              61 ccedecrecedcadedcadeccededcadcrc 91
                                                            433 CCGGGCTGCGGCAGGGCAGGGGGGGGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wakamatsu A,
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                                                                                                                                                                                            ВP
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2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                        (5'-primer)
                                                                                                                                                                                            AAH07432 standard; cDNA; 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99JP-0248036.
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                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       full-length cDNAs
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                                                                                                                                                                                                                                                                                                          Human cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                        EP1074617-A2
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                                                                                                                                                                                                                                  AAH07432;
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in the exemplification

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AAH18606

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represent oligonucleotides, all of which are used
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                         the present invention.
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                                                                                                                                        Local Similarity
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                                                                                                                      Query Match
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                                                                                                                                        Best Loc
Matches
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         22 X X S
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[11] Interpret cDNAS defined in the specification. Where a primer set

[12] Comprises: (a) an oligo-of primer and an oligonucleotide complementary

[13] Comprises: (b) an oligonaction which comprises one of

[14] Comprises at least 15 nucleotide which comprises one of

[15] Complementary strand of a polynucleotide which complementary to the

[16] Complementary strand of a polynucleotide which comprises a 5'-end

[17] Sequence and an oligonucleotide comprises a 5'-end

[18] Sequence and an oligonucleotide comprises a 5'-end

[19] Sequence and an oligonucleotide comprises a 5'-end

[20] Sequence and an oligonucleotide comprises a 5'-end

[21] Sequence and an oligonucleotide comprises a 5'-end

[22] Sequence and an oligonucleotide comprises a 5'-end

[23] Sequence and an oligonucleotide comprises a 5'-end

[24] Sequence and an oligonucleotide comprises a 5'-end

[25] Sequence and an oligonucleotide comprises a 5'-end

[26] Sequence and an oligonucleotide comprises and the complementary to a

[26] Sequence and an oligonucleotide comprises and the complementary to a

[27] Sequence and an oligonucleotide comprises and the complementary to a

[27] Sequence and an oligonucleotide comprises and the complementary to a

[28] Sequence and an oligonucleotide comprises and the complementary to a

[28] Sequence and an oligonucleotide comprises and the complementary to a

[28] Sequence and an oligonucleotide comprises and the complementary to a

[28] Sequence and an oligonucleotide comprises and the complementary to a

[29] Sequence and an oligonucleotide complementary to a

[20] Sequence and an oligonucleotide and the comple
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                                                                                              373 GTAATIGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTC 432
                                                      Gaps
                                                                                                                      Yamamote J;
                                                 C;
       DB 22; Length 736;
                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; SEQ ID 18808; 2537pp + CD ROM; English.
         Score 89.4; DB 22
Pred. No. 2.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sogai T, Nishikawa T, Hayashi K, S
Sugiyama I, Wakamatsu A, Nagai K,
                                                   0; Mismatches
                                                                                                                                                                                        433 CCGGGCTGCGCCAGGGCAGGCGGGAGCTC 463
                                                                                                                                                                                                               61 CCGGGCTGCGGCAGGCCAGGCGGGGGAGCTC 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA sequence SEQ ID NO:18808
                                                                                                                                                                                                                                                                                                                                                 AAH18606 standard; cDNA; 1556 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
         19.3%;
98.9%;
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                                                      90; Conservative
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              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ishii
                                                      Matches
                                                                                                                                                                                                                                                                                                    RESULT 12
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polyuucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the oligonucleotide which comprises a 1'-end sequence. Where the oligonucleotide which comprises a 1'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the
                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; primer: detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                             1 GIAGTIGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto J;
                                                                                                                                                0;
                                                                          Length 1556;
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                                                                                                                                                    Indels
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Sequence 1556 BP; 380 A; 363 C; 399 G; 414 T; 0 other;
                                                                          DB 22;
                                                                          Score 89.4; DB 22
Pred. No. 2.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID 1564; 2537pp + CD ROM; English.
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA clone (5'-primer) SEQ ID NO:1564.
                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               433 CCGGGCTGCGGCAGGGCGGGGGGGGGCTC 463
                                                                                                                                                                                                                                                                                                                                                                                                                             61 CCGGGCTGCGGCAGGCCAGGCCGGGAGCTC 91
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11-JAN-2000; 2000JP-0118776.
                                                                              19.3%;
98.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03165 to AAH13628 and AAH13633 to AAH18742 represent human cDNAs aguences; AAB92446 to AAH3893 represent human amino acid sequences, and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                         375 AATTECGAGCGAGAGIGAGIGGGGCCGGGACCCGCAGACCGAGCCGACCCTTCICTCCC 434
                                                                                                                                                                                                                                                         Yamamotc
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                                                                                                                                                                         Length 763;
                                                                                                                                                                                     3.3e-13;
nes 0; Indels
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Otsuki T;
                                                                                                                                       Sequence 763 BP; 137 A; 205 C; 250 G; 158 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; SEQ ID 16905; 2537pp + CD ROM; English.
                                                                                                                                                                       Score 89; DB 22;
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A, Nagai K,
                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                           435 GGGCTGCGGCAGGGCAGGCGGGGAGCTC 463
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAH17451 standard; cDNA; 1750 BP.
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                                                                                                                                                                     19.2%; Sc.
ilarity 100.0%; P:
Conservative 0;
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99JP-0300253.
2000JP-0118775.
2000JP-0183767.
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                                                                                                         the present invention.
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                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-2000;
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62-MAY-2000;
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Ishii S,
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the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy and primer sets can be used in antisense therapy and particularly full-length coNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length coNAs. The primers allow obtaining of the full-length coNAs. The primers allow obtaining of the full-length coNAs of the proteins encoded by the full-length coNAs. The primers allow obtaining of the full-length coNAs casily without any specialised methods. AAH0316 to AAH18628 and AAH18633 to AAH18628 con AAB95893 represent human coNA sequences; AAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy;
                                                                                                                                                         represent oligonucleotides, all of which are used in the exemplification
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                                                                                                                                                                                                                                                                                               375 AATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCC 434
                                                                                                                                                                                                                                                                                                                1 AATTGCGAGCGAGAGAGAGAGAGGGGCCGGGAACCGCAGAGCCGAGCCGAGCCAACCTTCTCTCCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopolesis: tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy
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Wang ZW;
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                                                                                                                                                                                                                                   Length 1750;
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Wang D, Wang J, Zhang J, Ren F, Chen R,
Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                    Sequence 1750 BP; 291 A; 489 C; 586 G; 384 T; 0 other;
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                                                                                                                                                                                                                                                  3.8e-13;
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                                                                                                                                                                                                                                   Score 89;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                            435 GGGCTGCGGCAGGGCAGGGGGGGAGCTC 463
                                                                                                                                                                                                                                                                                                                                                                                         89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human polynucleotide SEQ ID NO 228.
                                                                                                                                                                                                                                                                                                                                                                              ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK51683 standard; cDNA; 7281
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2000US-0560875.
2000US-0598075.
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2000US-0654936.
2000US-0663561.
2000US-0693325.
2000US-0728422.
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                                                                                                                                                                         the present invention.
                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAM78550
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The invention relates to polynuclectides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAW80302) that exhibit activity elating to excoded polypeptides (AAM78323-AAW80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The prolypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, cell growth factor activity, haematopoliesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, individual in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.

Content Records for SEO ID NO 2110 (AAK52561), 2111 (AAK52582) and 3566 (AAM80020) are omitted as the relevant pages from the sequence listing was activity and activity activity activity and activity activity activity activity and activity activity activity and activity activity activity and activity 
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0 Query Match 16.7%; Score 77.2; DB 22; Length 7281: Best Local Similarity 86.7%; Pred. No. 4.7e-10; Matches 85; Conservative 0; Mismatches 13; Indels 0; Sequence 7281 BP; 1831 A; 1773 C; 1915 G; 1762 T; C other;

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Search completed: February 3, 2003, 16:31:52 Job time: 226.594 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	<pre>February 3, 2003, 16:38:05 : Search time 1007.79 Seconds (without alignments) 10155.006 Million cell updates/sec</pre>
Title: Perfect score: Sequence:	US-09-596-141C-3_COPY_1292_1643 352 1 ggaccctaagacacctgctgcagggcagggggggggg
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post.processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : GenSmbl:*
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ensmbl:* gb_ba:* gb_htg:* gb_in:* gb_ow:* gb_ov:* gb_pat:*		em_nrs.: em_nrs.: em_hrg.] * em_hrg.] * em_hrg.] em_hrg.] em_hrg.] em_hrg.] em_hrg.] em_hrg.] em_hrg.] em_hrg.]
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ALIGNMENTS

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TOCUS	HSA252201 1167 bp DNA linear PRI 10-APR-2001
DEFINITION	Homo sapiens partial ABC-1 gene for ATP-binding cassette
	transporter-1, 5'UTR and promoter region.
ACCESSION	AJ252201
VERSION	AJ252201.1 GI:12053757
KEYWORDS	ABC-1 gene, ATP-binding cassette transporter-1; promoter.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1167)
AUTHORS	Porsch-Ozcurumez, M., Langmann, T., Heimerl, S., Borsukova, H.,
	Kaminski, W.E., Drobnik, W., Honer, C., Schumacher, C. and Schmitz, G.

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The zinc finger protein 202 (ZNF202) is a transcriptional repressor of ATP binding cassette transporter Al (ABCAL) and ABCG1 gene expression and a modulator of cellular lipid efflux 1. biol. Chem. 276 (15), 12427-12433 (2001)
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1 (bases 1 to 1643)
                                                                                           Direct Submission
Submitted (05-JAN-2000) Porsch-Oezcueruemez M.K., Institute for Submitted (05-JAN-2000) Voliversity of Regensburg, FRanz-Josef-Strauss-Allee II, 93042 Regensburg, GERMANY ICcation/Qualifiers
1...167
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100.0%; Pred. No. 2.5e-78;
Live 0; Mismatches 0;
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Eukaryota; Metazoa; Chordata; Craniata; Hominidae; Homo.
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Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
Artp binding cassette transporter protein abol polypeptides
Patent: WO 0079971-A 3 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
                 abc1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                 transporter protein
                                                                                                                                                                                              Indels
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                                                                                                                                                             100.0%; Score 352; DB 6; itarity 100.0%; Pred. No. 2.4e-78; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 352; DB 6; 100.0%; Pred. No. 2.4e-78;
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Lawn,R.M., Wade,D. and Garvin,M. Regulation with binding cassette tr Patent: WO 0078972-A 3 28-DEC-2030; CV THERAPEUTICS, INC. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403
                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9506"
a 413 c 457 g 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xxref="taxon:9606"
413 c 457 q 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3 from Patent WO0078971.
AX060894
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                                                                                                                                                                Query Match
Best Local S
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Op QΫ́ qq ΩŽ CD 92

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BASE COUNT
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lieut submission.

Diffect submission.

Diffect submission.

Cambridgeshire, CB10 18A, UK. E-mail enquiries:

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alterrate chemistry or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MIS subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given surface the Equire table with their source databases: Em; EMBL; SW;

SWISSPROT; Tr., TREMBL; Wp; WORMPEP; Information on the WORMPEP database can be found at the subcondition of the worm of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMPORTANT: This sequence is not the entire insert of clone RP11-21.787 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true right end of clone RP11-21787 is at 96717 in this sequence. The true left end of clone RP11-127810 is at 72980 in this sequence. The true right end of clone RP11-32710 is at 2000 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9. constructed by the Sanger Centre Caromosome 9 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL359182 96717 bp DNA linear PRI 11-JAN-2002 
Human DNA sequence from cione RP11-217B7 on chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/HGP/Chr9
RPI1-217B7 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                         241 ACTAGTCCCGGCAAAAACCCCGTAAITGCGAGCGAGAGTGAGTGGGGCCGGGAACCCGGAG 300
                                                                181 GAGCACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAATCTATAAAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCCGAGCCGACCCTTCTCTCTCCGGGCTGCGGCAGGCCAGGCCGGGGAGCTC 352
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VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL359182.20
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AC012230 175064 bp DNA linear HTG 22-APR-2000 Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered
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                                                                                                                                                                                                                                                                                                                              /note="Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Another "Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."

1 21138 c 20380 g 27526 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17458 TAGATGTGTGTGGGGGGGGGGGGGGCGGCCGGTTFAAGGGGGGGGCCCGGCTCCAGGG 17399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17398 CTTTCTGCTGAGTGACTGAACTACATAAACAGAGGCCGGGAACGGGGCGGGGAGGAGGGG 17339
                                                                                                                                                                                                                                                                                                       Assembly confirmed by restriction digest."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TAGATGTGTGGGCGGCGGCTGAACGTCGCCCGTTTAAGGGGCCGGGCCCCCGGGTCCACGTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                     Institutes of Heath, National Heart, Lung and Blood Institute, Bethesda, ND 20892, USA." 84273
Anote-"Sequence from overlapping clone RPII-122F10 (AC026643). Assembly confirmed by restriction dinast
                                                                                                                                  3238. 3278
/note="Sequence from AF275948 sequenced by National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 GAGCACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAATCTATAAAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 352; DB 9; Length 96717; 100.0%; Pred. No. 1.6e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 AGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGCAGGGCAGGGCGGGGAGCTC 352
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Birren, B., Linton, E., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-1M10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                     /clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC012230.3 GI:7637254
HTG; HTGS_PHASE1: HTGS_DRAFT.
Homo sapiens.
                                                                           /clone="RP11-21737"
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Matches 352; Conserv
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TITLE JOURNAL COMMENT

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ap of 100 bp contig of 11800 bp in length
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                                                                                                                                                                                                                                                                                                                             oof 100 bp
contig of 2943 bp in length
p of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                  63661: contig of 3926 bp in length 61: gap of 160 bp 68437: contig of 4676 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 bp
5125 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117308 117407; gap of 100 bp 117408 124019; contig of 6672 bp in length 12408 124179; gap of 100 bp in length 124180 132281; contig of 7102 bp in length
                                                                                                                                                                              p of 100 by contig of 2568 bp in length
                                                                                                                                                                                                                              p of 100 bp contig of 4402 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137: gap of 100 bp 71458: contig of 2921 bp in length
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5179 bp in length
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1. .1003
                                                                contly of 100 bp is contig of 4417 bp is not in 100 bp.
     34399: contig of 2861 bp
34399: gap of 100 bp
38318: contig of 3919 bp
                                                                                                                                                         contig of 2513 bp
                                                                                                                                                                                                                                                                                                    contig of 3874 bp
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/note="assembly_fragment"
5886. .7879
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9787. .12253
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12354. :15228
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15329. .17200
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7980. .9685
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/db_xref="taxon:9606"
/clone="RP11-1M10"
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52618:
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Ferreira, P., FirzHugh, W., Forrest, C., Funke, R., Gage, D., Galdgan, J., Gradyna, S., Grant, G., Hagos, B., Heaford, A., Horton, J., Howland, J.C., Johnson, R., Grant, G., Hagos, B., Heaford, A., Klein, J., Howland, J.C., Johnson, R., Macker, C., Kann, L., Karatas, A., Klein, J., McDewa, P., McGurk, A., McKernan, K., McLaughlin, J., Maldrim, J., McTawa, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Mortow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollar, V., Kley, R., Santos, R., Savery, P., Stange-Thomann, N., Stofanovic, N., Subramanlan, A., Talamas, J., Talamas, J., Talamas, J., Tariell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zlumer, A. and Zody, M.

Direct Submission

L. Submitted (21-OCT-1999) Whitehead Institute/WIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Apr 22, 2000 this sequence version replaced gi:6454033.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatWasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           center close name: 1_M_10

Sequencing vector: M13, M77815; 100% of reads
chemistry: Dye-terminator Big Dye; 100% of reads
chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
consensus quality: 117571 bases at least 040
consensus quality: 145749 bases at least 020
consensus quality: 160940 bases at least 020
Insert size: 185000; agarose-fp
Insert size: 171264; sum-of-contigs
Quality coverage: 2.9 in 020 bases; sum-of-contigs
Quality coverage: 3.2 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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31339 31438: gap of 100 bp
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of 1531 bp in length
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17200: contig of 1872 bp in length
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contig of 2875 bp in length
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25707: con
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5785: con
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9686: con
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5886 7879; co
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be preserved.
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Lyberto Submitted (120-ARR-2000) Cardiovascular Research Institute, University of California, San Francisco, 505 Parnassus Avenue, San Francisco, CA 94143-0130, USA
Francisco, CA 94143-0130, USA
3 (bases 1 to 1167)
52 Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,
Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
Direct Submission
AL Submitted (23-07N-2000) Cardiovascular Research Institute,
University of California, San Francisco, 505 Parnassus Avenue, San Francisco, CA 94143-0130, USA
Sequence update by submitter
On Jun 23, 2000 this sequence version replaced gi:7769713.
1 of 4 micro sapiens.
Homo sapiens .
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GAGCACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAATCTATAAAAGGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tallinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Analysis of hABC1 gene 5' end: additional peptide sequence, promoter region, and four polymorphisms
Biochem. Biophys. Res. Commun. 271 (2000) In press
2 (bases 224 to 1167)
Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
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/db_xref="taxon:9606"
/chromosome="9"
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845. .1147
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AF258623.2 GI:8677405
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34400. 38318
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9131: gap of 100 bp 4006: contig of 875 bp in length 4006: contig of 875 bp in length 4006; gap of 100 bp 100 bp 1007; gap of 100 bp 100 bp 100 bp 42013; contig of 846 bp in length 42824: contig of 811 bp in length
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                                                                                                                                                                      S Birren B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson.S. Baldwin,J. Barna,N., Beckerly,R., Beda,F., Boukngalter,B., Beckerly,R., Beda,F., Boukngalter,B., Brown,A., Burkt,G., Castle,A., Choepel,Y., Colangelo,K., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Domino,M., Doyle,M., Ferestor J., Ferrelra,P., Fiztung,M., Forrest,C., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Hagford,A., Forton,L., Macdona,S., Chinson,R., Jones,C., Kann,D., Karatas,A., Klein,J., Mardquis,N., McEwan,C., Liu,G., Locke,K., McChenan,Z., McPheerers,R., Melafim,J., Meneus,L., Morlow,J., Naylor,J., Norman,C.E., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K., Fierre,N., Fisanl,C., Pollara,V., Raymond,C., Riegy,R., Rothman,D., Stojanovic,N., Subramanian,A., Talamas,J., Tesfage,Thomann,N., Tirrell,A., Vassillev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J., Almers, A., And Cady,M.
                                                                                                                                                                                                                                                                                                                                                                                                                              Genome
                                                                                Eukaryota; Metazoa; Chordata; Cranista; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 13, 2000 this sequence version replaced 91:6705871. All trepeats were identified using RepeatMasker: Smit, A.P.A. & Green, P. (1996-1997)
                                                                                             Primates; Catarrhini; Hominidae; Homo
 sapiens clone RP11-1N10, LOW-PASS SEQUENCE SAMPLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is usefu. for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smit, A.F.A. & Green, P. (1990-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                will be sequenced to completion. In the event the the event the be preserved.
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of 851 bp in length
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f 844 bp in length
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f 800 bp in length
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f 870 bp in length
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome, clone RPI1-IN10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This record contains 73 individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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Center clone name: LN_10
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5741 6540: c
6541 6640: gap c
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7510 7609: gap c
                         AC021246.2 GI:9119882
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3745:
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                                        HTG; HTGS_PHASEO.
                                                       Homo sapiens
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PAT 21-MAR-2001
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                                                                                                                                                                                                     Vertebrata; Euteleostomi;
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Eukaryota; Metazoa; Chordana; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                28524 GGACCTAAGACACCTGCTGTACCCTCCANNCNNCNCCCCACCCACCCACCCCCCAA 28583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M. Compositions and methods for modulating hdl cholesterol and trigityceride levels

Batent: WO 0115676-A 1 08-MAR-2001;
University of British Columbia (CA) : Xenon Genetics Inc. (C
            240 AACTAGTCCCGGCAAAAACCCCGTAATTGCGAGCGAGAGTGGGGGCCGGGACCCGCA
                      28644 ACGIGCITICIGCIGAGIGACIGAACAAAAACAGAGGCCGGGAACGGGGCGGGGAGG
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                                                                                                                                                                                                              Catarrhini; Hominidae;
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/db_xref="taxon:9606"
37944 c 41170 g 54950 t
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Mammalia; Eutheria; Primates;
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AX092589.1 GI:13444647
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1852 bp in length
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of 864 bp in length
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f 852 bp in length
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f 834 bp in length
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855 bp in length
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contig of 875 bp in length
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contig of 840 bp in length
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53328: cont
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62865: cont
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7.12-2.4. 2598,40385. .40478,45012. .45153,46423. .46541, 67729. 67850. 70831. .71007,83960. .84052,80010. .89250, 67729. .6780. 70831. .71007,83960. .84052,80010. .89250, 67729. .6780. 70831. .71007,83960. .84052,80010. .89250, 98428. .98604,100391. .100613.10260. .102581.103642. .103642. .103644. .100391. .100943,100646. .103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 1103666, 11
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                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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8800. .9046
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9998. .10279
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18600. .18860
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20950. .21206
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:5508. .15787
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563. 5839
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5615. .6877
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1859. .12133
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2810. .12902
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5220. .15399
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5038. .25314
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1998. .5270
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                                                                                                                                                    1454. .148034
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                                                                Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P., Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S. Regulatory nucleic acid sequences of the abcl gene Patent: WO 0183746-A 1 08-NOV-2001; Aventis Pharma S.A. (FR)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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PCYVDDIFLRYMSRAPLEWILAWITSVAVIIKGIVVEKEABLKETMRIMGLDNSILM FSWFISSLIPLLVSAGLLVVILKLGNILPYSDPSVVEVELSVFAVVIILOCFIISTLF SRANLAAACGGIIYFTLYLPYVLCVAWODYVGFTLKIFAXLLSPVAFGFGCEYFALFE EQGIGVQWDNLFESPVEEDGFNLTTSVSMMLFDTFLYGVMTWYIEAVFPGQYGIPRPW YFPCTKSYWFGEESDEKSHPGSNQKRISEICMBEEFTHLKLGVSIQNLVKVYRDGMXV AVDGLALNFYEGQITSFLGHNGAGKTTTMSILIGLFPPTSGTAYILGKDIRSEMSTIR QNLGVCPOHNVLFDMLIVEEHIWFYARLKGLSEKHVKAEMEQMALDVGLPSSKLKSKT HHMDEADVLSDRIAIISHGKLCCVGSSLFLKNOLGTGYYLTLUKKDVESSLSSCRNSS STVSYLKKEDSVSGSSSDAGLGSDHESDTLTIDVSAISNLIRKHVSEARLVEDIGHEL TYVLPYEAAKEGAFYELFHEIDDRLSDLGISSYGISETTLEEIFLKVAEESGVDAETS GYGTPARRYRAFGBKQSCLRFFTEDDAADPNDSDIDPERFEYDLLGSYGYK GWKLTQOQCYALLWRKLLIARRSKGFFAQIYUPAVEYCIALVFSLIVPPFGKYPSLE LQPWXNEQYTFVSNDAAPEDTGTLELLNALTKDPGFGTRCMEGNFIPDTPQQAGBEEN NAILRANLOKGENPSHYGITAFNHPLNLFKOOLSEVAXMTTSVDVLVSICVITAMSFV PASFVVFLIQERVSKAKHLOFISGVKPVIYMLSNFVMDMCNYVVPATLVIIFICFQQ KSYVSSINLPVLALLLLLYGWSITPLMYPASFVFKIPSTAYVVLISVNLFIGINGSVA /translation="MACWPQLRLLLWKNLTFRRRQTCQLLLEVAWPLFIFLILISVRL SYPPYEQHECHFPNKAMPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIV ARLFSDARRLLLYSQKDTSMKDMRKVLRTEQQIKKSSSNLKLQDFLVDNBTFSGFLYH NLSLPKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEEMIQLGDQBVSELGGLP REKLAAAERVLRSNMDIJKPILRTINSTSPFPSKEJAEATKTLLHSLGTLAQELFSMR SWSDMRQEVWFLTNVNSSSSSTQIYQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALF GGNGTEEDAETFYDNSTTPYCNDLAKNLESSPLSRIIWKALKFLLVGKILYTPDTPAT RQVMAEVNKTFQELAVFHDLEGMWEELSPKIWTFMENSQEMDLVRMLLDSRDNDHFWE QQLDGLDW1AQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNQAIR1ISRFMECVNLN KLEPIATEVWLINKSWELLDERKFWAGIVFTGITPGSIELPHHVKYKIRWDIDNVERT NKIKDGYWDFGPRADPFEDMRYVWGGFAYLQDVYEQAIIRVLTGTEKKTGVYMQQMPY TTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLFVCPPGAGGLPPFQRKQNTA DILQDLIGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQEVN DAXKOMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLÑVIN TFVLELFTDNKLNNINDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVS PLSWDLVGRNLFAMAVECVVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQ RILDGGGGNBILEIKELTKIYRRKRYPAVDRICVGIPPGECFGLLGVNGAGKSSTFKM LIGDITVIRGDAFINXNSILSNIHEVHQNMGYCPQFDAITELLIGREHVEFFALLRGV PEKEVGKVGEWAIRKLGLVKYGEKYAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTG MDPKARRFLWNCAJSVVKEGRSVVLTSHSMEECEALCIRMAIMVNGRFRCLGSVQHLK NRFGDGYTIYVRIAGSNPDLKPYQDFFGLAFPGSVXFKHRNMLQYQLPSSLSYQHLK FSILSQSKKRLHIEDYSVSQTTLDQVFVNFAKDQSDDBHLKDLSLHKNQTVVDVAVLT SFLQDSKVKESYV" SQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLKYRQGRTIILST 29916. .30180 /rpt_family="Alu" 31050. 3131 /rpt_family="Alu" 37999. .apic /rpt_family="Alu"
31692 .31973
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7167 .36440
/rpt_family="Alu"
37617 .37892 /rpt_family="Alu" 38172. .38269 /rpt_family="Alu" 38995. .39271 /rpt_family="Alu" 41547. 41555 /gene="ABCAl" /rpt_family="Alu" 11657. .41679 /gene="ABCAl" /rpt_family="Alu" 44349. .44626 'rpt_family="Alu" /note="A009X28" 41593. 41835 /note="A009X28" .44626 .42584 42320. repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region

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Qiu.Y., Cavelier.L., Chiu.S., Yang.X., Rubin.E. and Cheng.J.F. Human and mouse ABCAL comparative sequencing and transgenesis
                                                                                                                                                                                                                                                                                                                                                                                                                             1248 CTCCCTAGATGTGTGTGGGGGGGGGGGGGGGGGCGGGCCGGGGCCGGGCTC 1307
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Genomics 73 (1), 66-76 (2001)
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Pred. No. 2.3e-74;
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                                                                                                                                /rpt_family="EERV"
61246. .61489
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55297. .55344
                                                                                      /rpt_family="Alu"
58501. .58935
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68499. .68731
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                                                                                                               'note="LTR"
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62812. .630
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69481. .697
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64082. .64
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Matches 351; Conserv
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AVOGLALNIYSEQITISFLGHNGAGKTTMSILIGLEPPTSGTAYILGXDIRSBNSTIR
QNLGVCPQHNVLFDMLTVEEHIWFYARLKGLSKKHVKAEMEDRALDVSIRSSKIKSKT
SQLSGGMORKLSVALAFVGGSKVVVILDBPTAGVDFYSRRGIWELLLKYRQGRTIILST
                                                                                                                                                                                                                    HMDZADVLGBRIAIISHGKLCCVGSSLFLKNQLGTGYYLTIVKKDVBSSLSSCRNSS
STVSYLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNLIRKHVSEARLVDDGHEL
TYVLPYEAAKBGAFVELFHEIDDRLSDLGISSYGISETTLEEIFLKVAEESGVDAETS
DGTLPARRNERAFGDKQSCLRPFTEDDAADPNDSDIDPESRETDLLSGMDGKGSYQVK
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LQPWWINEQYIFVSNDAPEDTGILELINALIKKDPGFGTRCMEGNPIPDTPCQACEEEW
TTAPVFQTIMDLFQNGNWTMQNPSPACQCSSDXIKKMLPVCPPGAGGLPPPQRKQNTA
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LIGDTTVTRGDAFLKKNSILSNIHEVHQNMGYCPQFDAITELLIGREHVEFFALLRGV
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NRFGDGYTIVVRIAGSNPDLKPVQDFFGLAFPGSVLKEKHRNMLQYQLPSSLSSLARI
                             EQGIGVQWDNLFESPVEEDGFNLTTSVSMMLFNTFLYGVMTWYIEAVFPGQYGIPRPW
                                                               YFPCTKSYWFGEESDEKSHPGSNQKRISEICMEEEPTHLKLGVSIQNLVKVYRDGMKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join (33931. 34151,58319. .58476,72893. .72996,77520. .77661,78931. .37049,10148. .101169,10152. .12986,77520. .77661,78232. .12569,125285. .12244,125754. .125764,125754. .125769,130276,131023. .131228,131749. .131925,131028. .133708. .133904,135677. .13898,131063. .131925,131063,13891,140179. .140350,141340. .141471,14134. .14519,14132. .14280,141340. .141471. .14519,14133. .142806,143963. .144183,14542. .14519,14150. .156891. .152078. .15202,155421. .155126. .15612. .160892,166598. .16679. .166792,166588. .166792,166588. .166792,166588. .166793,166792,166588. .166793,176992,170199. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .170109. .17010
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SYPPYEQHECHFPNKAMPSAGTLPWVQGIICNANNPCFRYPIPGEAPGVVGNFNKSIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARLF SDARRILLYSGKDTSKKDMRKYLRTLGQIKKS SSNLKLGDFLVDNETFSGFLYH
NLSLPKSTVDKMLRADVILHKVFLGGYQLHLTSLCNGSKSEBMIQLGDGEVSELGGLP
KEKLAAABERVLRSKMDILKPILRTLNSTSPFPSKELABATKIILHSLGTLAQELFSMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWSDMRQEVAPLINVNSSSSSTOIYOAVSALVCGHEEGGGLKIKSLMWYEDNNYKALF
GGNGTEEDAETFYDNSTTPYCNDLMKNLESSPLSRIIWKALKRLLVGKILYTPDTPAI
RQVMAEVNKTFQELAVFHDLEGMWEELSPKIWTFMENSQEMDLVRMILDSRDNDHFWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OQLDGLDWTAQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNOAIRTISRFMECVNLN
KLEPIATEVWLINKSMELLDERKFWAGIVFTGIT?GSIELPHHVKYKIRMDIDNVERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NKIKDGYWDDGPRADPPEDMRYWGGRAYLODVVBQAIIRVLTGTEKKTGVYMOOMPY
PCYYDDIFLRVMSRSMPJEMTLAWIYSVAVIIKGIVYBKEARLKETMRIMGLDNSILW
FSNWFISSLIPLIVSAGLLVVIIKLGNLLPYSDPSVVFVFLSVFAVYTILQCFLISTLE
SRANLAAACGGIIYFFLYLPYVLCVAWQDYVGFTJKIFASLLSPVAFGFGCECFALFE
                                                                        2 (bases 1 to 201144)
Olu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
Submitted (13-JUL-2000) Genome Science Department, Lawrence
Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-271, Berkeley,
CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="ATP-binding cassette 1 sub-family A member 1" 33931. .34151 /gene="ABCA1"
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/protein_id="AAK43526.1"
/db_xref="GI:13876613"
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                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
33931. .181457
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                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /qene="ABCAl
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                                      11352567
                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                       AUTHORS
                                                                                                                                                                                                        COURNAL
                                      PUBMED
                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
MEDLINE
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                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                         TITLE
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Dignorments of 9970)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barnan, N., Beckerly, R., Beda, F., Boduslavkiy, L., Boukhgalter, B., Erown, A., Burkett, G., Castle, A., Choepel, Y., Colangallo, M., Collins, S., Collymore, A., Cooke, P., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferrelra, P., Titzlugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Herford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehorckky, J., Levine, P., McGurk, A., McKernan, K., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, K., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassillev, H., Viel, R., Wo, X., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cararrini; Hominidae; Homo. 1 (bases 1 to 65570)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zimmer.A. and Zody,M.
Direct Submission
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 92141, USA
On Jul 13, 2000 this sequence version replaced g1:6705871.
All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Low pass sequence sampling is completely identifying clones that may be gene-fich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              872 971: gap of 100 bp 972 1834: contig of 863 bp in length 1835 1934: gap of 100 bp 1935 2804: contig of 870 bp in length
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                                                                                                                                                             Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome, clone RP11-1N10
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4696: contig of 851 bp
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Center clone name: 1_N_10
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contig of 846 bp in length
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Z1865: contig of 2
21965: qan of
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9009: contig of 9: gap of 1
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40967: con⊤
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28532: con
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Score 271.6; DB 2; Length 69570; Pred. No. 2.9e-58;); Mismatches 33; Indels 0; in length in length in length in length in length contig of 857 bp in length 20 of 100 bp contig of 844 bp in length in length in length length length length length in length in length in length in length is length 디 in in in ju ij in in 4652: gap of 100 bp 45724: contig of 872 bp in 46724: gap of 100 bp 46643: contig of 819 bp in 6743: gap of 100 bp 47599: contig of 856 bp in 47599: contig of 85699: con 1083: gap of 100 bp 100 7263: gap of 100 bp 58130: contig of 867 bp in 58230: gap of 100 bp 59082: contig of 852 bp in 5182: gap of 100 bp 56020: contig of 838 bp in 56020: up of 100 bp. contig of 834 bp in the of 100 bp. contig of 855 bp in the other of 855 bp in 1p of 100 bp |
contig of 861 bp i
1p of 100 bp |
contig of 868 bp i 84: gap of 100 bp 67651: contig of 867 bp 51: gap of 100 bp oof 100 bp contig of 852 bp 72: gap of 100 bp 53328: contig of 856 bp 28: gap of 100 bp 54268: contig of 840 bp 176: gap of 100 bp 44752: contig of 876 bp p of 100 bp contig of 864 bp 04: gap of 100 bp 52372: contig of 868 bp gap of 100 pp 53: contig of 866 bp 20: gap of 100 bp 60983: contig of 863 bp .: cont .u: gap of 55229: cr 0 55329: r /51: > 49485: cc.. 705: gap of con' .u: gap of 63827. .40: gap of 51404: con+ .99: gap of 48551: con 59182: gap of 60020: con 83: gap of 55740: con gap of 67751: gap of 77.2%; 57163: 66684 51504: 44852: Conservative 46743 52472: 53428: 58230: 62966: 50540 57263: 45824 48651 62035: 65840: 47699 61083 49585 56297 60120 63927 64883 54269 55330 56198 56298 Query Match Best Local Similarity 48652 49486 51405 51505 53329 57164 57264 438777 438777 44753 446853 45725 45825 45825 46644 47600 55230 59083 59183 60984 60021 289; Matches 151 91 67582 67522

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Sirven, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boquslavkiy, L., Bockigalter, B., Brown, A., Burket, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cocke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Howland, J.C., Johnson, R., Heador, R., McEnton, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Mardula, J., McDwan, P., McGurk, A., McEnan, K., McPheeters, R., Medrim, J., Menneus, L., Morrow, J., Naylor, J., Norman, C.E., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Pitani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Presson, R., Peterson, R., Peterso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassillev, E., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6705761.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
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Web site: http://www-seq.wi.mit.edu
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contig of 851 bp
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Center clone name: 24_J_9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zimmer, A. and Zody, M. Direct Submission
          (bases 1 to 90698)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brewer, B., Duverger, N., Ramaley, A. and Santamanna-Fojo, S.
Regulatory nucleic acid sequences of the abol gene
Patent: WO 0183746-A 3 08-NOV-2001;
Aventis Pharma S. A. (FR)
Loanion/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                  67402 ASCGAGAGAGAGAGGGGCGGGACCCGCAGAGCAGAGCCGACCTTTCTCTCCCGGTCTGC 67343
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Homo sapiens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING.
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Pred. No. 2.8e-51;
0; Mismatches 1; Indels 5;
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Pred. No. 4.7e-47;
0; Mismatches 27; Indels 3
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59075: contig of 854 bp in length
5975: gap of 100 bp
60088: contig of 883 bp in length
60158: gap of 100 bp
61067: contig of 909 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115: gap of 100 bp 65975: contig of 860 bp in length 65975: age of 100 bp 65941: contig of 893 bp in length 67947: contig of 893 bp in length 67947: contig of 893 bp in length
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69910: contig of 875 bp in length
70010: gap of 100 bp
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             1309: gap of 100 bp 52221: contig of 912 bp 10 5221: gap of 100 bp 53205: contig of 884 bp 10 54225: contig of 920 bp 10 54225: c
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dq 001
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f 881 bp
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58121: contig of 897
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15: gap of 100 b
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... gap of
62051: contig
7 62151: gap of
63022: c
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55206: cont
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Matches 275; Conservative
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RESULT 15 AF258627

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Homo sapiens AIP binding cassette transporter 1 (ABCA1) mRNA,
partial cds.
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198 c 190 g 156 t others
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O
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                                                                                                                                                  Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

Pullinger.C.R., Hakamata, H., Duchateau, P.N., Eng, C.,

Aouizerat, B.E., Fielding, C.J. and Kane, J.P.

Analysis of hARGI gene 5' end: additional peptide sequence, promoter region, and four polymorphisms

Biochem. Biophys. Res. Commun. 271 (2000) In press 2 (bases i to 697)

Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,

Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
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SOURCE
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